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(54) Title: NUCLEIC ACID VACCINES AGAINST RICKETTSIAL DISEASES AND METHODS OF USE

(57) Abstract: Described are nucleic acid vaccines containing genes to protect animals or humans against rickettsial diseases. Also described are polypeptides and methods of using these polypeptides to detect antibodies to pathogens.

DESCRIPTION

NUCLEIC ACID VACCINES AGAINST RICKETTSIAL DISEASES AND METHODS OF USE

This invention was made with government support under USAID Grant No. LAG-1328-G-00-3030-00. The government has certain rights in this invention.

Technical Field

This invention relates to nucleic acid vaccines for rickettsial diseases of animals, including humans.

Background of the Invention

The rickettsias are a group of small bacteria commonly transmitted by arthropod vectors to man and animals, in which they may cause serious disease. The pathogens causing human rickettsial diseases include the agent of epidemic typhus, *Rickettsia prowazekii*, which has resulted in the deaths of millions of people during wartime and natural disasters. The causative agents of spotted fever, *e.g.*, *Rickettsia rickettsii* and *Rickettsia conorii*, are also included within this group. Recently, new types of human rickettsial disease caused by members of the tribe *Ehrlichiae* have been described. *Ehrlichiae* infect leukocytes and endothelial cells of many different mammalian species, some of them causing serious human and veterinary diseases. Over 400 cases of human ehrlichiosis, including some fatalities, caused by *Ehrlichia chaffeensis* have now been reported. Clinical signs of human ehrlichiosis are similar to those of Rocky Mountain spotted fever, including fever, nausea, vomiting, headache, and rash.

Heartwater is another infectious disease caused by a rickettsial pathogen, namely *Cowdria ruminantium*, and is transmitted by ticks of the genus *Amblyomma*. The disease occurs throughout most of Africa and has an estimated endemic area of about 5 million square miles. In endemic areas, heartwater is a latent infection in indigenous breeds of cattle that have been subjected to centuries of natural selection. The problems occur where the disease contacts susceptible or naive cattle and other ruminants. Heartwater has been confirmed to be on the island of Guadeloupe in the Caribbean and is spreading through the Caribbean Islands. The tick vectors responsible for spreading this disease are already present on the American mainland and threaten the livestock industry in North and South America.

In acute cases of heartwater, animals exhibit a sudden rise in temperature, signs of anorexia, cessation of rumination, and nervous symptoms including staggering, muscle twitching, and convulsions. Death usually occurs during these convulsions. Peracute cases of the disease occur where the animal collapses and dies in convulsions having shown no preliminary symptoms. Mortality is high in susceptible animals. Angora sheep infected with the disease have a 90% mortality rate while susceptible cattle strains have up to a 60% mortality rate.

If detected early, tetracycline or chloramphenicol treatment are effective against rickettsial infections, but symptoms are similar to numerous other infections and there are no satisfactory diagnostic tests (Helmick, C., K. Bernard, L. D'Angelo [1984] *J. Infect. Dis.* 150:480).

Animals which have recovered from heartwater are resistant to further homologous, and in some cases heterologous, strain challenge. It has similarly been found that persons recovering from a rickettsial infection may develop a solid and lasting immunity. Individuals recovered from natural infections are often immune to multiple isolates and even species. For example, guinea pigs immunized with a recombinant *R. conorii* protein were partially protected even against *R. rickettsii* (Vishwanath, S., G. McDonald, N. Watkins [1990] *Infect. Immun.* 58:646). It is known that there is structural variation in rickettsial antigens between different geographical isolates. Thus, a functional recombinant vaccine against multiple isolates would need to contain multiple epitopes, *e.g.*, protective T and B cell epitopes, shared between isolates. It is believed that serum antibodies do not play a significant role in the mechanism of immunity against rickettsia (Uilenberg, G. [1983] *Advances in Vet. Sci. and Comp. Med.* 27:427-480; Du Plessis, Plessis, J.L. [1970] *Onderstepoort J. Vet. Res.* 37(3):147-150).

Vaccines based on inactivated or attenuated rickettsiae have been developed against certain rickettsial diseases, for example against *R. prowazekii* and *R. rickettsii*. However, these vaccines have major problems or disadvantages, including undesirable toxic reactions, difficulty in standardization, and expense (Woodward, T. [1981] "Rickettsial diseases: certain unsettled problems in their historical perspective," In *Rickettsia and Rickettsial Diseases*, W. Burgdorfer and R. Anacker, eds., Academic Press, New York, pp. 17-40).

A vaccine currently used in the control of heartwater is composed of live infected sheep blood. This vaccine also has several disadvantages. First, expertise is required for the intravenous inoculation techniques required to administer this vaccine. Second, vaccinated animals may experience shock and so require daily monitoring for a period after vaccination. There is a possibility of death due to shock throughout this monitoring period, and the drugs

needed to treat any shock induced by vaccination are costly. Third, blood-borne parasites may be present in the blood vaccine and be transmitted to the vaccinates. Finally, the blood vaccine requires a cold chain to preserve the vaccine.

Clearly, a safer, more effective vaccine that is easily administered would be particularly advantageous. For these reasons, and with the advent of new methods in biotechnology, investigators have concentrated recently on the development of new types of vaccines, including recombinant vaccines. However, recombinant vaccine antigens must be carefully selected and presented to the immune system such that shared epitopes are recognized. These factors have contributed to the search for effective vaccines.

A protective vaccine against rickettsiae that elicits a complete immune response can be advantageous. A few antigens which potentially can be useful as vaccines have now been identified and sequenced for various pathogenic rickettsia. The genes encoding the antigens and that can be employed to recombinantly produce those antigen have also been identified and sequenced. Certain protective antigens identified for *R. rickettsii*, *R. conorii*, and *R. prowazekii* (*e.g.*, rOmpA and rOmpB) are large (>100 kDa), dependent on retention of native conformation for protective efficacy, but are often degraded when produced in recombinant systems. This presents technical and quality-control problems if purified recombinant proteins are to be included in a vaccine. The mode of presentation of a recombinant antigen to the immune system can also be an important factor in the immune response.

Nucleic acid vaccination has been shown to induce protective immune responses in non-viral systems and in diverse animal species (Special Conference Issue, WHO meeting on nucleic acid vaccines [1994] *Vaccine* 12:1491). Nucleic acid vaccination has induced cytotoxic lymphocyte (CTL), T-helper 1, and antibody responses, and has been shown to be protective against disease (Ulmer, J., J. Donelly, S. Parker *et al.* [1993] *Science* 259:1745). For example, direct intramuscular injection of mice with DNA encoding the influenza nucleoprotein caused the production of high titer antibodies, nucleoprotein-specific CTLs, and protection against viral challenge. Immunization of mice with plasmid DNA encoding the *Plasmodium yoelii* circumsporozoite protein induced high antibody titers against malaria sporozoites and CTLs, and protection against challenge infection (Sedegah, M., R. Hedstrom, P. Hobart, S. Hoffman [1994] *Proc. Natl. Acad. Sci. USA* 91:9866). Cattle immunized with plasmids encoding bovine herpesvirus 1 (BHV-1) glycoprotein IV developed neutralizing antibody and were partially protected (Cox, G., T. Zamb, L. Babiuk [1993] *J. Virol.* 67:5664). However, it has been a question in the field of immunization whether the recently discovered technology of nucleic acid vaccines can provide improved protection against an antigenic drift variant. Moreover, it has

not heretofore been recognized or suggested that nucleic acid vaccines may be successful to protect against rickettsial disease or that a major surface protein conserved in rickettsia was protective against disease.

Brief Summary of the Invention

Disclosed and claimed here are novel vaccines for conferring immunity to rickettsia infection, including *Cowdria ruminantium* causing heartwater. Also disclosed are novel nucleic acid compositions and methods of using those compositions, including to confer immunity in a susceptible host. Also disclosed are novel materials and methods for diagnosing infections by *Ehrlichia* in humans or animals.

One aspect of the subject invention concerns a nucleic acid, *e.g.*, DNA or mRNA, vaccine containing the major antigenic protein 1 gene (MAP1) or the major antigenic protein 2 gene (MAP2) of rickettsial pathogens. In one embodiment, the nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. In studies immunizing mice by intramuscular injection of a DNA vaccine composition according to the subject invention, immunized mice seroconverted and reacted with MAP1 in antigen blots. Splenocytes from immunized mice, but not from control mice immunized with vector only, proliferated in response to recombinant MAP1 and rickettsial antigens in *in vitro* lymphocyte proliferation tests. In experiments testing different DNA vaccine dose regimens, increased survival rates as compared to controls were observed on challenge with rickettsia. Accordingly, the subject invention concerns the discovery that DNA vaccines can induce protective immunity against rickettsial disease or death resulting therefrom.

The subject invention further concerns the genes designated *Cowdria ruminantium map 2*, *Cowdria ruminantium 1hworf3*, *Cowdria ruminantium 4hworf1*, *Cowdria ruminantium 18hworf1*, and *Cowdria ruminantium 3gdorf3* and the use of these genes in diagnostic and therapeutic applications. The subject invention further concerns the proteins encoded by the exemplified genes, antibodies to these proteins, and the use of such antibodies and proteins in diagnostic and therapeutic applications.

In one embodiment of the subject invention, the polynucleotide vaccines are administered in conjunction with an antigen. In a preferred embodiment, the antigen is the polypeptide which is encoded by the polynucleotide administered as the polynucleotide vaccine. As a particularly preferred embodiment, the antigen is administered as a booster subsequent to the initial administration of the polynucleotide vaccine.

Brief Description of the Drawings

Figures 1A-1C show a comparison of the amino acid sequences from alignment of the three rickettsial proteins, namely, *Cowdria ruminantium* (*C.r.*), *Ehrlichia chaffeensis* (*E.c.*), and *Anaplasma marginale* (*A.m.*).

Figures 2A-2C shows the DNA sequence of the 28 kDa gene locus cloned from *E. chaffeensis* (Fig. 2A-2B) and *E. canis* (Fig. 2C). One letter amino acid codes for the deduced protein sequences are presented below the nucleotide sequence. The proposed sigma-70-like promoter sequences (38) are presented in bold and underlined text as -10 and -35 (consensus -35 and -10 sequences are TTGACA and TATAAT, respectively). Similarly, consensus ribosomal binding sites and transcription terminator sequences (bold letter sequence) are identified. G-rich regions identified in the *E. chaffeensis* sequence are underlined. The conserved sequences from within the coding regions selected for RT-PCR assay are identified with italics and underlined text.

Figure 3A shows the complete sequence of the MAP2 homolog of *Ehrlichia canis*. The arrow (➜) represents the predicted start of the mature protein. The asterisk (*) represents the stop codon. Underlined nucleotides 5' to the open reading frame with -35 and -10 below represent predicted promoter sequences. Double underlined nucleotides represent the predicted ribosomal binding site. Underlined nucleotides 3' to the open reading frame represent possible transcription termination sequences.

Figure 3B shows the complete sequence of the MAP2 homolog of *Ehrlichia chaffeensis*. The arrow (➜) represents the predicted start of the mature protein. The asterisk (*) represents the stop codon. Underlined nucleotides 5' to the open reading frame with -35 and -10 below represent predicted promoter sequences. Double underlined nucleotides represent the predicted ribosomal binding site. Underlined nucleotides 3' to the open reading frame represent possible transcription termination sequences.

Brief Description of the Sequences

SEQ ID NO. 1 is the coding sequence of the MAP1 gene from *Cowdria ruminantium* (Highway isolate).

SEQ ID NO. 2 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 1.

SEQ ID NO. 3 is the coding sequence of the MAP1 gene from *Ehrlichia chaffeensis*.

SEQ ID NO. 4 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 3.

SEQ ID NO. 5 is the *Anaplasma marginale* MSP4 gene coding sequence.

SEQ ID NO. 6 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 5.

SEQ ID NO. 7 is a partial coding sequence of the VSA1 gene from *Ehrlichia chaffeensis*, also shown in Figures 2A-2B.

SEQ ID NO. 8 is the coding sequence of the VSA2 gene from *Ehrlichia chaffeensis*, also shown in Figures 2A-2B.

SEQ ID NO. 9 is the coding sequence of the VSA3 gene from *Ehrlichia chaffeensis*, also shown in Figures 2A-2B.

SEQ ID NO. 10 is the coding sequence of the VSA4 gene from *Ehrlichia chaffeensis*, also shown in Figures 2A-2B.

SEQ ID NO. 11 is a partial coding sequence of the VSA5 gene from *Ehrlichia chaffeensis*, also shown in Figures 2A-2B.

SEQ ID NO. 12 is the coding sequence of the VSA1 gene from *Ehrlichia canis*, also shown in Figure 2C.

SEQ ID NO. 13 is a partial coding sequence of the VSA2 gene from *Ehrlichia canis*, also shown in Figure 2C.

SEQ ID NO. 14 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 7, also shown in Figures 2A-2B.

SEQ ID NO. 15 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 8, also shown in Figures 2A-2B.

SEQ ID NO. 16 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 9, also shown in Figures 2A-2B.

SEQ ID NO. 17 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 10, also shown in Figures 2A-2B.

SEQ ID NO. 18 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 11, also shown in Figures 2A-2B.

SEQ ID NO. 19 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 12, also shown in Figure 2C.

SEQ ID NO. 20 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 13, also shown in Figure 2C.

SEQ ID NO. 21 is the coding sequence of the MAP2 gene from *Ehrlichia canis*, also shown in Figure 3A.

SEQ ID NO. 22 is the coding sequence of the MAP2 gene from *Ehrlichia chaffeensis*, also shown in Figure 3B.

SEQ ID NO. 23 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 21, also shown in Figure 3A.

SEQ ID NO. 24 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 22, also shown in Figure 3B.

SEQ ID NO. 25 is the coding sequence of the *map2* gene from *Cowdria ruminantium*.

SEQ ID NO. 26 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 25.

SEQ ID NO. 27 is the coding sequence of the *ihworf3* gene from *Cowdria ruminantium*.

SEQ ID NO. 28 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 27.

SEQ ID NO. 29 is the coding sequence of the *4hworf1* gene from *Cowdria ruminantium*.

SEQ ID NO. 30 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 29.

SEQ ID NO. 31 is the coding sequence of the *18hworf1* gene from *Cowdria ruminantium*.

SEQ ID NO. 32 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 31.

SEQ ID NO. 33 is the coding sequence of the *3gdorf3* gene from *Cowdria ruminantium*.

SEQ ID NO. 34 is the polypeptide encoded by the polynucleotide of SEQ ID NO. 33.

Detailed Disclosure of the Invention

In one embodiment, the subject invention concerns a novel strategy, termed nucleic acid vaccination, for eliciting an immune response protective against rickettsial disease. The subject invention also concerns novel compositions that can be employed according to this novel strategy for eliciting a protective immune response.

According to the subject invention, recombinant DNA or mRNA encoding an antigen of interest is inoculated directly into the human or animal host where an immune response is induced. Prokaryotic signal sequences may be deleted from the nucleic acid encoding an antigen of interest. Advantageously, problems of protein purification, as can be encountered with antigen delivery using live vectors, can be virtually eliminated by employing the compositions or methods according to the subject invention. Unlike live vector delivery, the subject invention can provide a further advantage in that the DNA or RNA does not replicate in the host, but remains episomal. See, for example, Wolff, J.A., J.J. Ludike, G. Acsadi, P. Williams, A. Jani (1992) *Hum. Mol. Genet.* 1:363. A complete immune response can be obtained as recombinant antigen is synthesized intracellularly and presented to the host immune system in the context of autologous class I and class II MHC molecules.

In one embodiment, the subject invention concerns nucleic acids and compositions comprising those nucleic acids that can be effective in protecting an animal from disease or death caused by rickettsia. For example, a nucleic acid vaccine of the subject invention has been

shown to be protective against *Cowdria ruminantium*, the causative agent of heartwater in domestic ruminants. Accordingly, nucleotide sequences of rickettsial genes, as described herein, can be used as nucleic acid vaccines against human and animal rickettsial diseases.

In one embodiment of the subject invention, the polynucleotide vaccines are administered in conjunction with an antigen. In a preferred embodiment, the antigen is the polypeptide which is encoded by the polynucleotide administered as the polynucleotide vaccine. As a particularly preferred embodiment, the antigen is administered as a booster subsequent to the initial administration of the polynucleotide vaccine. In another embodiment of the invention, the polynucleotide vaccine is administered in the form of a "cocktail" which contains at least two of the nucleic acid vaccines of the subject invention. The "cocktail" may be administered in conjunction with an antigen or an antigen booster as described above.

The MAP1 gene, which can be used to obtain this protection, is also present in other rickettsiae including *Anaplasma marginale*, *Ehrlichia canis*, and in a causative agent of human ehrlichiosis, *Ehrlichia chaffeensis* (van Vliet, A., F. Jongejan, M. van Kleef, B. van der Zeijst [1994] *Infect. Immun.* 62:1451). The MAP1 gene or a MAP1-like gene can also be found in certain *Rickettsia* spp. MAP1-like genes from *Ehrlichia chaffeensis* and *Ehrlichia canis* have now been cloned and sequenced. These MAP-1 homologs are also referred to herein as Variable Surface Antigen (VSA) genes.

The present invention also concerns polynucleotides encoding MAP2 or MAP2 homologs from *Ehrlichia canis* and *Ehrlichia chaffeensis*. MAP2 polynucleotide sequences of the invention can be used as vaccine compositions and in diagnostic assays. The polynucleotides can also be used to produce the MAP2 polypeptides encoded thereby.

The subject invention further concerns the genes designated *Cowdria ruminantium map 2*, *Cowdria ruminantium 1hworf3*, *Cowdria ruminantium 4hworf1*, *Cowdria ruminantium 18hworf1*, and *Cowdria ruminantium 3gdorf3* and the use of these genes in diagnostic and therapeutic applications. The subject invention further concerns the proteins encoded by the exemplified genes, antibodies to these proteins, and the use of such antibodies and proteins in diagnostic and therapeutic applications.

Compositions comprising the subject polynucleotides can include appropriate nucleic acid vaccine vectors (plasmids), which are commercially available (*e.g.*, Vical, San Diego, CA). In addition, the compositions can include a pharmaceutically acceptable carrier, *e.g.*, saline. The pharmaceutically acceptable carriers are well known in the art and also are commercially available. For example, such acceptable carriers are described in E.W. Martin's *Remington's Pharmaceutical Science*, Mack Publishing Company, Easton, PA.

The subject invention also concerns polypeptides encoded by the subject polynucleotides. Specifically exemplified are the polypeptides encoded by the MAP-1 and VSA genes of *C. rumimontium, E. chaffeensis. E. canis* and the MP4 gene of *Anaplasma marginale*. Polypeptides uncoded by *E. chaffeensis* and *E. canis* MAP2 genes are also exemplified herein.

Also encompassed within the scope of the present invention are fragments and variants of the exemplified polynucleotides and polypeptides. Fragments would include, for example, portions of the exemplified sequences wherein procaryotic signal sequences have been removed. Examples of the removal of such sequences are given in Example 3. Variants include polynucleotides and/or polypeptides having base or amino acid additions, deletions and substitutions in the sequence of the subject molecule so long as those variants have substantially the same activity or serologic reactivity as the native molecules. Also included are allelic variants of the subject polynucleotides. The polypeptides of the present invention can be used to raise antibodies that are reactive with the polypeptides disclosed herein. The polypeptides and polynucleotides can also be used as molecular weight markers.

Another aspect of the subject invention concerns antibodies reactive with MAP-1 and MAP2 polypeptides disclosed herein. Antibodies can be monoclonal or polyclonal and can be produced using standard techniques known in the art. Antibodies of the invention can be used in diagnostic and therapeutic applications.

In a specific embodiment, the subject invention concerns a DNA vaccine (*e.g.*, VCL1010/MAP1) containing the major antigenic protein 1 gene (MAP1) driven by the human cytomegalovirus (HCMV) enhancer-promoter. In a specific example, this vaccine was injected intramuscularly into 8-10 week-old female DBA/2 mice after treating them with 50 μl/muscle of 0.5% bupivacaine 3 days previously. Up to 75% of the VCL1010/MAP1-immunized mice seroconverted and reacted with MAP1 in antigen blots. Splenocytes from immunized mice, but not from control mice immunized with VCL1010 DNA (plasmid vector, Vical, San Diego) proliferated in response to recombinant MAP1 and *C. ruminantium* antigens in *in vitro* lymphocyte proliferation tests. These proliferating cells from mice immunized with VCL1010/MAP1 DNA secreted IFN-gamma and IL-2 at concentrations ranging from 610 pg/ml and 152 pg/ml to 1290 pg/ml and 310 pg/ml, respectively. In experiments testing different VCL1010/MAP1 DNA vaccine dose regimens (25-100 μg/dose, 2 or 4 immunizations), survival rates of 23% to 88% (35/92 survivors/total in all VCL1010/MAP1 immunized groups) were observed on challenge with 30LD50 of *C. ruminantium*. Survival rates of 0% to 3% (1/144 survivors/total in all control groups) were recorded for control mice immunized similarly with VCL1010 DNA or saline. Accordingly, in a specific embodiment, the subject invention

concerns the discovery that the gene encoding the MAP1 protein induces protective immunity as a DNA vaccine against rickettsial disease.

The nucleic acid sequences described herein have other uses as well. For example, the nucleic acids of the subject invention can be useful as probes to identify complementary sequences within other nucleic acid molecules or genomes. Such use of probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is needed. As is well known in the art, probes can be made by labeling the nucleic acid sequences of interest according to accepted nucleic acid labeling procedures and techniques. A person of ordinary skill in the art would recognize that variations or fragments of the disclosed sequences which can specifically and selectively hybridize to the DNA of rickettsia can also function as a probe. It is within the ordinary skill of persons in the art, and does not require undue experimentation in view of the description provided herein, to determine whether a segment of the claimed DNA sequences is a fragment or variant which has characteristics of the full sequence. *e.g.*, whether it specifically and selectively hybridizes or can confer protection against rickettsial infection in accordance with the subject invention. In addition, with the benefit of the subject disclosure describing the specific sequences, it is within the ordinary skill of those persons in the art to label hybridizing sequences to produce a probe.

Various degrees of stringency of hybridization can be employed. The more severe the conditions, the greater the complementarity that is required for duplex formation. Severity of conditions can be controlled by temperature, probe concentration, probe length, ionic strength, time, and the like. Preferably, hybridization is conducted under moderate to high stringency conditions by techniques well known in the art, as described, for example, in Keller, G.H., M.M. Manak (1987) *DNA Probes*. Stockton Press, New York, NY., pp. 169-170.

Examples of various stringency conditions are provided herein. Hybridization of immobilized DNA on Southern blots with 32P-labeled gene-specific probes can be performed by standard methods (Maniatis *et al.* (1982) *Molecular Cloning: A Laboratory Manual*. Cold Spring Harbor Laboratory, New York.). In general, hybridization and subsequent washes can be carried out under moderate to high stringency conditions that allow for detection of target sequences with homology to the exemplified polynucleotide sequence. For double-stranded DNA gene probes, hybridization can be carried out overnight at 20-25° C below the melting temperature (Tm) of the DNA hybrid in 6X SSPE, 5X Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. The melting temperature is described by the following formula (Beltz et al.

et al. [1983] *Methods of Enzymology*, R. Wu, L. Grossman and K. Moldave [eds.] Academic Press, New York 100:266-285).

Tm=81.5°C+16.6 Log[Na+]+0.41(%G+C)-0.61(%formamide)-600/length of duplex in base pairs.

Washes are typically carried out as follows:

(1) twice at room temperature for 15 minutes in 1X SSPE, 0.1% SDS (low stringency wash);

(2) once at Tm-20°C for 15 minutes in 0.2X SSPE, 0.1% SDS (moderate stringency wash).

For oligonucleotide probes, hybridization can be carried out overnight at 10-20°C below the melting temperature (Tm) of the hybrid in 6X SSPE, 5X Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. Tm for oligonucleotide probes can be determined by the following formula:

Tm (°C)=2(number T/A base pairs) +4(number G/C base pairs) (Suggs *et al.* [1981] *ICN-UCLA Symp. Dev. Biol. Using Purified Genes*, D.D. Brown [ed.], Academic Press, New York, 23:683-693).

Washes can be carried out as follows:

(1) twice at room temperature for 15 minutes 1X SSPE, 0.1% SDS (low stringency wash;

(2) once at the hybridization temperature for 15 minutes in 1X SSPE, 0.1% SDS (moderate stringency wash).

In general, salt and/or temperature can be altered to change stringency. With a labeled DNA fragment >70 or so bases in length, the following conditions can be used:

Low:	1 or 2X SSPE, room temperature
Low:	1 or 2X SSPE, 42°C
Moderate:	0.2X or 1X SSPE, 65°C
High:	0.1X SSPE, 65°C.

Duplex formation and stability depend on substantial complementarity between the two strands of a hybrid and, as noted above, a certain degree of mismatch can be tolerated. Therefore, the probe sequences of the subject invention include mutations (both single and multiple), deletions, insertions of the described sequences, and combinations thereof, wherein said mutations, insertions and deletions permit formation of stable hybrids with the target polynucleotide of interest. Mutations, insertions and deletions can be produced in a given

polynucleotide sequence in many ways, and these methods are known to an ordinarily skilled artisan. Other methods may become known in the future.

It is also well known in the art that restriction enzymes can be used to obtain functional fragments of the subject DNA sequences. For example, *Bal*31 exonuclease can be conveniently used for time-controlled limited digestion of DNA (commonly referred to as "erase-a-base" procedures). See, for example, Maniatis *et al.* (1982) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York; Wei *et al.* (1983) *J. Biol. Chem.* 258:13006-13512.

In addition, the nucleic acid sequences of the subject invention can be used as molecular weight markers in nucleic acid analysis procedures.

Following are examples which illustrate procedures for practicing the invention. These examples should not be construed as limiting. All percentages are by weight and all solvent mixture proportions are by volume unless otherwise noted.

Example 1

A nucleic acid vaccine construct was tested in animals for its ability to protect against death caused by infection with the rickettsia *Cowdria ruminantium*. The vaccine construct tested was the MAP1 gene of *C. ruminantium* inserted into plasmid VCL1010 (Vical, San Diego) under control of the human cytomegalovirus promoter-enhancer and intron A. In this study, seven groups containing 10 mice each were injected twice at 2-week intervals with either 100, 75, 50, or 25 μg VCL1010/MAP1 DNA (V/M in Table 1 below), or 100, 50 μg VCL1010 DNA (V in Table 1) or saline (Sal.), respectively. Two weeks after the last injections, 8 mice/group were challenged with 30LD50 of *C. ruminantium* and clinical symptoms and survival monitored. The remaining 2 mice/group were not challenged and were used for lymphocyte proliferation tests and cytokine measurements. The results of the study are summarized in Table 1, below:

Table 1

	100 μg V/M	75 μg V/M	50 μg V/M	25 μg V/M	100 μg V	50 μg V	Sal.
Survived	5	7	5	3	0	0	0
Died	3	1	3	5	8	8	8

The VCL1010/MAP1 nucleic acid vaccine increased survival on challenge in all groups, with a total of 20/30 mice surviving compared to 0/24 in the control groups.

This study was repeated with another 6 groups, each containing 33 mice (a total of 198 mice). Three groups received 75 µg VCL1010/MAP1 DNA or VCL1010 DNA or saline (4 injections in all cases). Two weeks after the last injection, 30 mice/group were challenged with 30LD50 of *C. ruminantium* and 3 mice/group were sacrificed for lymphocyte proliferation tests and cytokine measurements. The results of this study are summarized in Table 2, below:

Table 2

	V/M 2 inj.	V 2 inj.	Sal. 2 inj.	V/M 4 inj.	V 4 inj.	Sal. 4 inj.
Survived	7	0	0	8	0	1
Died*	23	30	30	22	30	29

*In mice that died in both V/M groups, there was an increase in mean survival time of approximately 4 days compared to the controls ($p<0.05$).

Again, as summarized in Table 2, the VCL1010/MAP1 DNA vaccine increased the numbers of mice surviving in both immunized groups, although there was no apparent benefit of 2 additional injections. In these two experiments, there were a cumulative total of 35/92 (38%) surviving mice in groups receiving the VCL1010/MAP1 DNA vaccine compared to 1/144 (0.7%) surviving mice in the control groups. In both immunization and challenge trials described above, splenocytes from VCL1010/MAP1 immunized mice, but not from control mice, specifically proliferated to recombinant MAP1 protein and to *C. ruminantium* in lymphocyte proliferation tests. These proliferating splenocytes secreted IL-2 and gamma-interferon at concentrations up to 310 and 1290 pg/ml respectively. These data show that protection against rickettsial infections can be achieved with a DNA vaccine. In addition, these experiments show MAP1-related proteins as vaccine targets.

<u>Example 2 – Cloning and sequence analysis of MAP1 homologue genes of *E. chaffeensis* and *E. canis*</u>

Genes homologous to the major surface protein of *C. ruminantium* MAP1 were cloned from *E. chaffeensis* and *E. canis* by using PCR cloning strategies. The cloned segments represent a 4.6 kb genomic locus of *E. chaffeensis* and a 1.6 kb locus of *E. canis*. DNA sequence generated from these clones was assembled and is presented along with the deduced amino acid

sequence in Figures 2A-2B (SEQ ID NOs. 7-11 and 14-18) and Figure 2C (SEQ ID NOs. 12-13 and 19-20). Significant features of the DNA include five very similar but nonidentical open reading frames (ORFs) for *E. chaffeensis* and two very similar, nonidentical ORFs for the *E. canis* cloned locus. The ORFs for both *Ehrlichia* spp. are separated by noncoding sequences ranging from 264 to 310 base pairs. The noncoding sequences have a higher A+T content (71.6% for *E. chaffeensis* and 76.1% for *E. canis*) than do the coding sequences (63.5% for *E. chaffeensis* and 68.0% for *E. canis*). A G-rich region -200 bases upstream from the initiation codon, sigma-70-like promoter sequences, putative ribosome binding sites (RBS), termination codons, and palindromic sequences near the termination codons are found in each of the *E. chaffeensis* noncoding sequences. The *E. canis* noncoding sequence has the same feature except for the G-rich region (Figure 2C; SEQ ID NOs. 12-13 and 19-20).

Sequence comparisons of the ORFs at the nucleotide and translated amino acid levels revealed a high degree of similarity between them. The similarity spanned the entire coding sequences, except in three regions where notable sequence variations were observed including some deletions/insertions (Variable Regions I, II and III). Despite the similarities, no two ORFs are identical. The cloned ORF 2, 3 and 4 of *E. chaffeensis* have complete coding sequences. The ORF1 is a partial gene having only 143 amino acids at the C-terminus whereas the ORF5 is nearly complete but lacks 5-7 amino acids and a termination codon. The cloned ORF2 of *E. canis* also is a partial gene lacking a part of the C-terminal sequence. The overall similarity between different ORFs at the amino acid level is 56.0% to 85.4% for *E. chaffeensis*, whereas for *E. canis* it is 53.3%. The similarity of *E. chaffeensis* ORFs to the MAP1 coding sequences reported for *C. ruminantium* isolates ranged from 55.5% to 66.7%, while for *E. canis* to *C. ruminantium* it is 48.5% to 54.2%. Due to their high degree of similarity to MAP1 surface antigen genes of *C. ruminantium* and since they are nonidentical to each other, the *E. chaffeensis* and *E. canis* ORFs are referred to herein as putative Variable Surface Antigen (VSA) genes. The apparent molecular masses of the predicted mature proteins of *E. chaffeensis* were 28.75 kDa for VSA2, 27.78 for VSA3, and 27.95 for VSA4, while *E. canis* VSA1 was slightly higher at 29.03 kDa. The first 25 amino acids in each VSA coding sequence were eliminated when calculating the protein size since they markedly resembled the signal sequence of *C. ruminantium* MAP1 and presumably would be absent from the mature protein.

The amino acid sequence derived from the cloned *E. chaffeensis* MAP1-like gene, and alignment with the corresponding genes of *C. ruminantium* and *A. marginale* is shown in Figure 1.

Example 3

A further aspect of the subject invention are five additional genes which give protection when formatted as DNA vaccines. These genes are *Cowdria ruminantium map 2*, *Cowdria ruminantium 1hworf3*, *Cowdria ruminantium 4hworf1*, *Cowdria ruminantium 18hworf1*, and *Cowdria ruminantium 3gdorf3*. The DNA and translated amino acid sequences of these five genes are shown in SEQ ID NOS. 25-34.

There is published information showing that gene homologs of all five genes are present in other bacteria. For example, a homolog of *map2* is present in *Anaplasma marginale*, a homolog of *1hworf3* is present in *Brucella abortus*, homologs of *4hworf1* are present in *Pseudomonas aeruginosa* and *Coxiella burnetii*, and homologs of *18hworf1* are present in *Coxiella burnetii* and *Rickettsia prowazekii*. This can be revealed by a search of DNA and protein databases with standard search algorithms such as "Blast". Based on the protective ability of these genes against *Cowdria ruminantium* and their presence in other bacterial pathogens, the subject invention further concerns the use of these genes, their gene products, and the genes and gene products of the homologs as vaccines against bacteria. This includes their use as DNA or nucleic acid vaccines or when formulated in vaccines employing other methods of delivery, *e.g.*, recombinant proteins or synthetic peptides in adjuvants, recombinant live vector delivery systems such as vaccinia (or other live viruses) or *Salmonella* (or other live bacteria). These methods of delivery are standard to those familiar with the field. This also includes vaccines against heartwater disease, vaccines against rickettsial diseases in general and vaccines against other bacteria containing homologs of these genes.

Table 3 shows the protective ability of the 5 genes against death from *Cowdria ruminantium* challenge in mice. Genes were inserted into VR1012 according to the manufacturers instructions (Vical, San Diego) and challenge studies were conducted as described in Example 1. N-terminal sequences which putatively encoded prokaryotic signal peptides were deleted because of the potential for their affects on expression and and immune responses in eukaryotic expression systems or challenged animals. The inserts were as follows: map2, SEQ ID NO. 25, beginning at base 46; 18hworf1, SEQ ID NO. 31, beginning at base 67; 3gdorf3, SEQ ID NO. 33, beginning at base 79; lhworf3, SEQ ID NO. 27, beginning at base 76; and 4hworf1, SEQ ID NO. 29, beginning at base 58.

Table 3

DNA Construct	MWT Size	Survival Rate				
		Vaccinated		Control		P value
TMMAP 2	21 kd	9/28*	32%	0/29	0%	0.004
MB18HWORF1	28 kd	10/30*	33%	1/27	4%	0.021
AM3GDORF3	16 kd	7/26	27%	1/27	4%	0.060
TM1HWORF3	36 kd	8/29	28%	2/30	7%	0.093
TM4HWORF1	19 kd	10/30*	33%	2/30	7%	0.054

Control - VR1012 DNA vector plasmid only

*Statistically significant difference (Fisher's Exact test)

It should be understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and the scope of the appended claims.

Claims

1. A composition comprising a polynucleotide which encodes a polypeptide having the characteristic of eliciting an immune response protective against disease or death caused by a rickettsial pathogen.

2. The composition, according to claim 1, wherein said rickettsial pathogen is selected from the group consisting of *Rickettsia* spp., *Ehrlichia* spp., *Anaplasma* spp., and *Cowdria* spp.

3. The composition, according to claim 1, wherein said polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 14, SEQ ID NO. 15, SEQ ID NOS. 16-20, SEQ ID NO. 23, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, homologs thereof, and immunogenic fragments thereof.

4. The composition, according to claim 1, wherein said polynucleotide has a nucleic acid sequence selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NOS. 9-13, SEQ ID NO. 21, SEQ ID NO. 22,, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, homologs thereof, and fragments thereof which encode immunogenic polypeptides.

5. The composition, according to claim 4, wherein said polynucleotide has a nucleic acid sequence of SEQ ID NO. 3, or a fragment thereof.

6. The composition, according to claim 1, wherein said polynucleotide further comprises a nucleic acid vaccine vector.

7. The composition, according to claim 1, further comprising a pharmaceutically acceptable carrier.

8. A polynucleotide encoding a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO. 4, SEQ ID NOS. 14-20, SEQ ID NOS. 23-24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, and fragments thereof.

9. The polynucleotide, according to claim 8, said polynucleotide having a nucleic acid sequence selected from the group consisting of SEQ ID NO. 3, SEQ ID NOS. 7-13, SEQ ID NOS. 21-22, SEQ ID NOS. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, and SEQ ID NO. 33.

10. A method for protecting a susceptible host against disease or death caused by a rickettsial pathogen, said method comprising administering an effective amount of a polynucleotide encoding polypeptide having the characteristic of eliciting an immune response protective against said rickettsial pathogen.

11. The method, according to claim 10, wherein said rickettsial pathogen is selected from the group consisting of *Rickettsia* spp., *Ehrlichia* spp., *Anaplasma* spp., and *Cowdria* spp.

12. The method, according to claim 10, wherein said polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 14, SEQ ID NO. 15, SEQ ID NOS. 16-20, SEQ ID NO. 23, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, or homologs thereof and immunogenic fragments thereof.

13. The method, according to claim 10, wherein said polynucleotide has a nucleic acid sequence selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NOS. 9-13, SEQ ID NO. 21, SEQ ID NO. 22, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, and SEQ ID NO. 33.

14. The method, according to claim 13, wherein said polynucleotide has the nucleic acid sequence of SEQ ID NO. 1.

15. The method, according to claim 13, wherein said polynucleotide has the nucleic acid sequence of SEQ ID NO. 3.

16. The method, according to claim 13, wherein said polynucleotide has the nucleic acid sequence of SEQ ID NO. 5.

17. The method, according to claim 10, wherein said nucleic acid further comprises an appropriate nucleic acid vector.

18. The method, according to claim 10, wherein said composition further comprises a pharmaceutically acceptable carrier.

19. The method, according to claim 10, which further comprises administration to said host of said polypeptide encoded by said polypeptide.

20. A method for detecting, in a human or animal, antibodies associated with infection by *Ehrlichia*, wherein said method comprises contacting a biological fluid from said human or animal with a polypeptide selected from the group consisting of SEQ ID NO. 4, SEQ ID NOS. 14-20, SEQ ID NOS. 23-24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, and homologs and fragments thereof.

21. A method of detecting the presence of rickettsial nucleic acids comprising contacting a sample suspected of containing rickettsial nucleic acids with a composition comprising a labeled polynucleotide which encodes a polypeptide having the characteristic of eliciting an immune response protective against disease or death caused by a rickettsial pathogen, allowing for the formation of a hybridization complex and detecting said label.

22. The composition, according to claim 21, wherein said rickettsial pathogen is selected from the group consisting of *Rickettsia* spp., *Ehrlichia* spp., *Anaplasma* spp., and *Cowdria* spp.

23. The composition, according to claim 21, wherein said polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 14, SEQ ID NO. 15, SEQ ID NOS. 16-20, SEQ ID NO. 23, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, and homologs and immunogenic fragments thereof.

24. The composition, according to claim 21, wherein said polynucleotide has a nucleic acid sequence selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NOS. 9-13, SEQ ID NO. 21, SEQ ID NO. 22, , SEQ

ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, homologs thereof, and fragments thereof which encode immunogenic polypeptides.

FIG. 1A

```
C.r.    ATGAATTGCAAGAAAATTTTTA-------------TCACAAGTACACTAATATCATTAGTG
E.c.    ATGAATTACAAAAAAAGTTTCA--------------TAACAGCG-ATTGATATCATTAATA
A.m.    ATGAATTACAGAGAATTGTTTACAGGGGGCCTG-TCAGCAGCC-ACAGTCTGCGCCTGCT
        ******* **   **   ** *              *  **   *       *

C.r.    TCATTTT--TACCTGGTGTGTCCTTTTCTGATGTAATACAGGAAGACAGCAACCCAGCAG
E.c.    TCCTTCTCTTACCTGGAGTATCATTTTCCGACCCAAGGCAGGTAGTGGTCA---TTAACG
A.m.    CCCTACTTGTTAGTGGGGCCGTAGTGGCATCTCCCATGAGTCACGAAGTGGCTTCTGAAG
         * *  *  *   *** *      *  *       *        *              *

C.r.    GCAGTGTTTACATTAGCGCAAAATACATGCCAACTGCATCACATTTTGGTAAAATGTCAA
E.c.    GTAATTTCTACATCAGTGGAAAATACGATGCCAAGGCTTCGCATTTTGGAGTATTCTCTG
A.m.    GGGGAGTAATGGGAGGTAGCTTTTACGTGGGTGCGGCCT-ACAGCCCAGCATTTCCTTCT
        *     *        *       ***         ** *  **     *        *

C.r.    TCAAAGAAGATTCAAAAAATACTCAAACGGTATTTGGTCTAAAAAAAGATTGGGATGGCG
E.c.    CTAAGGAAGAAAGAAATACAACAGTTGGAGTGTTTGGACTGAAGCAAAATTGGGACGGAA
A.m.    GTTACCTCGTTCGACATGCGTGAGTCAAGCAAAGAGACCTCA--TACGTTAGAGGCTATG
           *    *    * *                   *  ** *   *   *  *  *

C.r.    TTAAAACACCATCAGATTCTAGCAATACTAATTCTACAATTTTTACTGAAAAAGACTATT
E.c.    GCGCAATATC--CAACTCCTCCCCAAACGA-------TGTATTCACTGTCTCAAATTATT
A.m.    ACAAGAGCATTGCAACGATTGATGTGAGTGTGCCAGCAAACTTTTCCAAATCTGGCTACA
             *      **     *      *              **  *          **

C.r.    CTTTCAGATATGAAAACAATCCGTTTTTAGGTTTCGCTGGAGCAATTGGGTACTCAATGA
E.c.    CATTTAAATATGAAAACAACCCGTTTTTAGGTTTTGCAGGAGCTATTGGTTACTCAATGG
A.m.    CTTTTGCCTTCTCTAAAAACTTAATCACGTCTTTCGACGGCGCTGTGGGATATTCTCTGG
        * **    *     ** **     *      *** *  ** **  * ** ** **  **
```

FIG. 1B

```
C.r.  ATGGACCAAGAATAGAGTTCGAAGTATCCTATGAAACTTTTGATGTAAAAAACCTAGGTG
E.c.  ATGGTCCAAGAATAGAGCTTGAAGTATCTTATGAAACATTTGATGTAAAAAATCAAGGTA
A.m.  GAGGAGCCAGAGTGGAATTGGAAGCGAGCTACAGAAGGTTTGCTACTTTGGCGGACGGGC
        **  * *** * **  * ****     **   **  **** *            **

C.r.  GCAACTATAAAAACAACGCACACATGTACTGTGCTTTAGATACAGCAGCACAAAATAGCA
E.c.  ACAATTATAAGAATGAAGCACATAGATATTGTGCTCTATCCCATAACTCAGCAGCAGACA
A.m.  AGTACGCAAAAAGTG---------------GTGCGGAATCTCTGGCAGCTATTACCCGCG
         *    ** *                  ****   *          *         *

C.r.  CTAATGGCGCAGGATTAACTACATCTGTTATGGTAAAAAACGAAAATTTAACAAATATAT
E.c.  TGAGTAGTGCAAG---TAATAATTTTGTCTTTCTAAAAAATGAAGGATTACTTGACATAT
A.m.  ACGCTAACATTACTGAGACCAATTACTTCGTAGTCAAAATTGATGAAATCACAAACACCT
          *            *  *  *   *  *  * ****  **     *     * *  *

C.r.  CATTAATGTTAAATGCGTGTTATGATATCATGCTTGATGGAATACCAGTTTCTCCATATG
E.c.  CATTTATGCTGAACGCATGCTATGACGTAGTAGGCGAAGGCATACCTTTTTCTCCTTATA
A.m.  CAGTCATGTTAAATGGCTGCTATGACGTGCTGCACACAGATTTACCTGTGTCCCCGTATG
      ** * *** * ** *  ** *****  *  *       *   ****  * ** ** ***

C.r.  TATGTGCAGGTATTGGCACTGACTTAGTGTCAGTAATTAATGCTACAAATCCTAAATTAT
E.c.  TATGCGCAGGTATCGGTACTGATTTAGTATCCATGTTTGAAGCTACAAATCCTAAAATTT
A.m.  TATGTGCCGGGATAGGCGCAAGCTTTGTTGACATCTCTAAGCAAGTAACCACAAAGCTGG
      **** ** ** ** **  *    ** **     *   * *      **   * **  *

C.r.  CTTATCAAGGAAAGCTAGGCATAAGTTACTCAATCAATTCTGAAGCTTCTATCTTTATCG
E.c.  CTTACCAAGGAAAGTTAGGTTTAAGCTACTCTATAAGCCCAGAAGCTTCTGTGTTTATTG
A.m.  CCTACAGGGGCAAGGTTGGGATTAGCTACCAGTTTACTCCGGAAATATCCTTGGTGGCAG
      * **    ** *** * **  * ** ***    * *   * ***   **  *  *    *
```

FIG. 1C

```
C.r.    GTGGACATTTCCATAGAGTTATAGGTAATGAATTTAAAGATATTGCTACCTTAAAAATAT
E.c.    GTGGGCACTTTCATAAGGTAATAGGGAACGAATTTAGAGATATTCCTACTATAATACCTA
A.m.    GTGGGTTCTACCACGGGCTATTTGATGAGTCTTACAAGGACATTCCCGCACACAACAGTG
        ****    *  **     *  * *   *    *  *  ** *** *  *    *

C.r.    TTACTTCAAAAACAGGAATATCTAATCCTGGCTTTGCATCAGCAACACTTGATGTTTGTC
E.c.    CTGGATCAACACTTGCAGGAAAAGGAAACTACCCTGCAATAGTAATACTGGATGTATGCC
A.m.    TAAAGTTCTCTGGAGAAGCAAAA------------GCCTCAGTCAAAGCGCATATTGCTG
             *        * *  *               **   **  * *    ** *

C.r.    ACTTTGGTATAGAAATTGGAGGAAGGTTTGTATTTTAA---
E.c.    ACTTTGGAATAGAAATGGGAGGAAGGTTTAA----------
A.m.    ACTACGGCTTTAACCTTGGAGCAAGATTCCTGTTCAGCTAA
        ***  **  *  *  * **** *** **
```

```
   1 ggaatgaattcagggacatttctactcttaaagcgtttgctacaccatcatctgcagcta
       N  E  F  R  D  I  S  T  L  K  A  F  A  T  P  S  S  A  A  T
  61 ctccagacttagcaacagtaacactgagtgtgtgtccactttggagtagaacttggaggaa
       P  D  L  A  T  V  T  L  S  V  C  H  F  G  V  E  L  G  G  R
 121 gatttaacttctaatttttattacttgccacatgttaaaaataatctaaacttgtttttcatt
       F  N  F  *
 181 attgctacaaataaataaaatagtggcaaaaaaatgtagcaataagaggggggggggga
 241 ctaattactatctgccatatcccttactaccacttacactaaataatctgacaaatacaa
 301 cagcttctggagaaataaacaatatttaaatttttcttacaaaaaccatttatatccttgc
                                                      -35
 361 actaaaaactagcttataacttgtttttacattgtaggtttactactgttaatttgtttt
                    -10
 421 cactatttcaggtgtaatatgaactgcgaaaaatttttataacaactgcattaacatta
               RBS      M  N  C  E  K  F  F  I  T  T  A  L  T  L
 481 ctaatgtccttcttacctggaatatcactttctgatccagtacaggatgacaacattagt
     L  M  S  F  L  P  G  I  S  L  S  D  P  V  Q  D  D  N  I  S
 541 ggtaatttctacatcagtggaaagtatatgccaagcgcttcgcattttggagtttttct
     G  N  F  Y  I  S  G  K  Y  M  P  S  A  S  H  F  G  V  F  S
 601 gccaaggaagaaagaaatacaacagttggagtatttggaatagagcaagattgggataga
     A  K  E  E  R  N  T  T  V  G  V  F  G  I  E  Q  D  W  D  R
 661 tgtgtaatatctagaaccactttaagcgatatattcaccgttccaaattattcatttaag
     C  V  I  S  R  T  T  L  S  D  I  F  T  V  P  N  Y  S  F  K
 721 catgaaaacaatctattttcaggatttgcaggagctattggctactcaatggatggccca
     Y  E  N  N  L  F  S  G  F  A  G  A  I  G  Y  S  M  D  G  P
 781 agaatagagcttgaagtatctTatgaagcattcgatgttaaaaatcaaggtaacaattat
     R  I  E  L  E  V  S  Y  E  A  F  D  V  K  N  Q  G  N  N  Y
 841 aagaacgaagcacatagatattatgctctgtcccatcttctcggcacagagacacagata
     K  N  E  A  H  R  Y  Y  A  L  S  H  L  L  G  T  E  T  Q  I
 901 gatggtgcaggcagtgcgtctgtctttctaataaatgaaggactacttgataaatcattt
     D  G  A  G  S  A  S  V  F  L  I  N  E  G  L  L  D  K  S  F
 961 atgctgaacgcatgttatgatgtaataagtgaaggcatacctttttctccttatatatgt
     M  L  N  A  C  Y  D  V  I  S  E  G  I  P  F  S  P  Y  I  C
1021 gcaggtattggtattgatttagtatccatgtttgaagctataaatcctaaaatttcttat
     A  G  I  G  I  D  L  V  S  M  F  E  A  I  N  P  K  I  S  Y
1081 caaggaaaattaggcttaagttaccctataagcccagaagcttctgtgtttattggtgga
     Q  G  K  L  G  L  S  Y  P  I  S  P  E  A  S  V  F  I  G  G
1141 cattttcataaggtgataggaaacgaatttagagatattcctactatgatacctagtgaa
     H  F  H  K  V  I  G  N  E  F  R  D  I  P  T  M  I  P  S  E
1201 tcagcgcttgcaggaaaaggaaactaccctgcaatagtaacactggacgtgttctacttt
     S  A  L  A  G  K  G  N  Y  P  A  I  V  T  L  D  V  F  Y  F
1261 ggcatagaacttggaggaaggtttaactttcaactttgattattgccacaataaataaaa
     G  I  E  L  G  G  R  F  N  F  Q  L  *
1321 atagtggcaaaagaatgtagcaataagagggggagggggaactaaattattatttgcc
1381 atatcccttactaccacttacaccaaataatctgacaaatacaacagttcaaacaaaggt
1441 aaacaattcttaaatttgtcttatgagaaccattgatatcttatattaaaaactagctta
                                         -35
1501 taacttgtctttacattgcagttctactattgttaatttattttcactatttaggtgta
     -10                                                   RBS
1561 atatgaattgcaaaaaatttttataacaactgcattagtatcactaatgtcctttctac
       M  N  C  K  K  F  F  I  T  T  A  L  V  S  L  M  S  F  L  P
1621 ctggaatatcatttctgatccagtgcaaggtgacaatattagtggtaatttctatgtta
       G  I  S  F  S  D  P  V  Q  G  D  N  I  S  G  N  F  Y  V  S
1681 gtggcaagtatatgccaagtgcttcgcattttggcatgtttctgccaaagaagaaaaa
       G  K  Y  M  P  S  A  S  H  F  G  M  F  S  A  K  E  E  K  N
1741 atcctactgttgcattgtatggcttaaaacaagattgggaagggattagctcatcaagtc
       P  T  V  A  L  Y  G  L  K  Q  D  W  E  G  I  S  S  S  S  H
1801 acaatgataatcatttcaataacaagggttattcatttaaatatgaaaataacccatttt
       N  D  N  H  F  N  N  K  G  Y  S  F  K  Y  E  N  N  P  F  L
1861 tagggtttgcaggagctattggttattcaatgggtggtccaagagtagagtttgaagtgt
       G  F  A  G  A  I  G  Y  S  M  G  G  P  R  V  E  F  E  V  S
1921 cctatgaaacatttgacgttaaaaatcagggtaataactataaaaatgatgctcacagat
       Y  E  T  F  D  V  K  N  Q  G  N  N  Y  K  N  D  A  H  R  Y
1981 actgtgctttaggtcaacaagacaacagcggaatacctaaaactagtaaatacgtactgt
       C  A  L  G  Q  Q  D  N  S  G  I  P  K  T  S  K  Y  V  L  L
2041 taaaaagcgaaggattgcttgacatatcatttatgctaaatgcatgctatgatataataa
       K  S  E  G  L  L  D  I  S  F  M  L  N  A  C  Y  D  I  I  N
2101 acgagagcatacctttgtctccttacatatgtgcaggtgttggtActgatttaatatcca
       E  S  I  P  L  S  P  Y  I  C  A  G  V  G  T  D  L  I  S  M
2161 tgtttgaagctacaaatcctaaaatttcttaccaagggaagttaggtctaagttactcta
       F  E  A  T  N  P  K  I  S  Y  Q  G  K  L  G  L  S  Y  S  I
2221 taaacccagaagcttctgtacttattggtggacattttcataaggtgataggaaacgaat
       N  P  E  A  S  V  F  I  G  G  H  F  H  K  V  I  G  N  E  F
2281 ttagggacattcctactctgaaagcatttgttacgtcatcagctactccagatctagcaa
       R  D  I  P  T  L  K  A  F  V  T  S  S  A  T  P  D  L  A  I
```

FIG. 2A

```
2341 cagcaacactaagtgtatgtcattttggaatagaacttggaggaaggtttaacttttaat
      V  T  L  S  V  C  H  F  G  I  E  L  G  G  R  F  N  F  *
2401 tttgttattgccacatgttaaaaataatctaaacttgttttcattattgctacagtaaat
2461 aaaaatagtggcaaaagaatgtagcaataagaaggggggggggactaaattgctattt
2521 accatatcccttattataccacttacactaaataacttgacaaatacaacagctttctgga
2581 aaaacaaacaatacttaaatttctcttacaaaaaccatttatatctttgtactaaaaacta
                                           -35
2641 gcttataacttgtttttacattgtagttctactattgctaatttattttcactattttag
        -10
2701 gtgcaatatgaattgcaaaaaatttttttataacaactacattagtatcgctaatgtcctt
     RBS    M  N  C  K  K  F  F  I  T  T  T  L  V  S  L  M  S  P
2761 cttacctggaatatcattttctgatgcagtacagaacgacaatgttggtggtaatttcta
      L  P  G  I  S  F  S  D  A  V  Q  N  D  N  V  G  G  N  F  Y
2821 tatcagtgggaaatatgtaccaagtgtttcacattttggcgtattctctgctaaacagga
      I  S  G  K  Y  V  P  S  V  S  H  F  G  V  F  S  A  K  Q  E
2881 aagaaatacaacaatcggagtatttggattaaagcaagattgggatggcagcacaatatc
      R  N  T  T  I  G  V  F  G  L  K  Q  D  W  D  G  S  T  I  S
2941 caaaaattctcccagaaaatacatttaacgttccaaattattcatttaaatatgaaaataa
      K  N  S  P  E  N  T  F  N  V  P  N  Y  S  F  K  Y  E  N  N
3001 tccatttctaggttttgcaggagctgttggttatttaatgaatggtccaagaatagagtt
      P  F  L  G  F  A  G  A  V  G  Y  L  M  N  G  P  R  I  E  L
3061 agaaatgtcctatgaaacatttgatgtgaaaaaccagggtaataactataagaacgatgc
      E  M  S  Y  E  T  F  D  V  K  N  Q  G  N  N  Y  K  N  D  A
3121 tcacaaatattatgctttaacccataacagtgggggaaagctaagcaatgcaggtgataa
      H  K  Y  Y  A  L  T  H  N  S  G  G  K  L  S  N  A  G  D  K
3181 gtttgctttttctaaaaaatgaaggactacttgatatatcacttatgttgaatgcatgcta
      F  V  F  L  K  N  E  G  L  L  D  I  S  L  M  L  N  A  C  Y
3241 tgatgtaataagtgaaggaatacctttctctccttacatatgtgcaggtgttggtactga
      D  V  I  S  E  G  I  P  F  S  P  Y  I  C  A  G  V  G  T  D
3301 tttaatatccatgtttgaagctataaacccctaaaatttcttatcaaggaaagttaggttt
      L  I  S  M  F  E  A  I  N  P  K  I  S  Y  Q  G  K  L  G  L
3361 gagttactccataagcccagaagcttctgtttttgttggtggacatttccataaggtgat
      S  Y  S  I  S  P  E  A  S  V  F  V  G  G  H  F  H  K  V  I
3421 agggaatgaattcagagatattcctgctatgatacccagtacctcaactctcacaggtaa
      G  N  E  F  R  D  I  P  A  M  I  P  S  T  S  T  L  T  G  N
3481 tcactttactatagtaacactaagtgtatgccactttggagtggaacttggaggaaggtt
      H  F  T  I  V  T  L  S  V  C  H  F  G  V  E  L  G  G  R  F
3541 taacttttaattttattattgccacatgttaaaaataatctaaacttgtttttattattg
      N  F: *
3601 ctgcaggtaaataaaaatagtggcaaaagaatgtagcaataagaggggggggggactag
3661 tttataagtgctgtttttctcacctttacacatgatactatacttaaccagtttttttgc
3721 tattacttacctgacgtaatatattaaatttccttacaaaagttaccgatactttatac
                                                  -35
3781 aaaaatttatattctgacttgcttttatatgacacttctactattgttaatttatttgtc
            -10
3841 actattaggttatatatgaattacaaaaaagttttcataacaagtgcattgatatcatta
           RBS     M  N  Y  K  K  V  F  I  T  S  A  L  I  S  L
3901 atatcttctctacctggagtatcattttccgacccagcaggtagtggtattaacggtaat
     I  S  S  L  P  G  V  S  F  S  D  P  A  G  S  G  I  N  G  N
3961 ttctacatcagtggaaaatacatgccaagtgcttcgcattttggagtattctctgctaag
     F  Y  I  S  G  K  Y  M  P  S  A  S  H  F  G  V  F  S  A  K
4021 gaagaaagaaatacaacagttggagtgtttggactgaagcaaaattgggacggaagcgca
     E  E  R  N  T  T  V  G  V  F  G  L  K  Q  N  W  D  G  S  A
4081 atatccaactcctccccaaacgatgtattcactgtctcaaattattcatttaaatatcaa
     I  S  N  S  S  P  N  D  V  F  T  V  S  N  Y  S  F  K  Y  E
4141 aacaacccgtttttaggttttgcaggagctattggttactcaatggatggtccaagaata
     N  N  P  F  L  G  F  A  G  A  I  G  Y  S  M  D  G  P  R  I
4201 gagcttgaagtatcttatgaaacatttgatgtaaaaaatcaaggtaacaattataagaat
     E  L  E  V  S  Y  E  T  F  D  V  K  N  Q  G  N  N  Y  K  N
4261 gaagcacatagatattgtgctctatcccataactcagcagcagacatgagtagtgcaagt
     E  A  H  R  Y  C  A  L  S  H  N  S  A  A  D  M  S  S  A  S
4321 aataatttgtctttctaaaaaatgaaggattacttgacatatcatttatgctgaacgca
     N  N  F  V  F  L  K  N  E  G  L  L  D  I  S  F  M  L  N  A
4381 tgctatgacgtagtaggcgaaggcatacctttttctccttatatatgcgcaggtatcggt
     C  Y  D  V  V  G  E  G  I  P  F  S  P  Y  I  C  A  G  I  G
4441 actgatttagtatccatgtttgaagctacaaatcctaaaatttcttaccaaggaaagtta
     T  D  L  V  S  M  F  E  A  T  N  P  K  I  S  Y  Q  G  K  L
4501 ggtttaagctactctataagcccagaagcttctgtgtttattggtgggcactttcataag
     G  L  S  Y  S  I  S  P  E  A  S  V  F  I  G  G  H  F  H  K
4561 gtaatagggaacgaatttagagatattcctactataatacctactggatcaacacttgca
     V  I  G  N  E  F  R  D  I  P  T  I  I  P  T  G  S  T  L  A
4621 ggaaaaggaaactaccctgcaatagtaatactggatgtatgccactttggaatagaaatg
     G  K  G  N  Y  P  A  I  V  I  L  D  V  C  H  F  G  I  E  M
4681 gga
     G
```

FIG. 2B

```
   1 tggtgtaaatatgaaatataaaaaaacttttacagtaactgcattagtattattaacttc
     RBS        M  K  Y  K  K  T  F  T  V  T  A  L  V  L  L  T  S
  61 ctttacacatttataccttttttatagtccagcacgtgccagtacaattcacaacttcta
      F  T  H  F  I  P  F  Y  S  P  A  R  A  S  T  I  H  N  F  Y
 121 cattagtggaaaatatatgccaacagcgtcacatttggaatttttcagctaaagaaga
      I  S  G  K  Y  M  P  T  A  S  H  F  G  I  F  S  A  K  E  E
 181 acaaagttttactaaggtattagcttgggttagatcaacgattatcacataatattataaa
      Q  S  F  T  K  V  L  V  G  L  D  Q  R  L  S  H  N  I  I  N
 241 caataatgatacagcaaagagtcttaaggttcaaaattattcatttaaatacaaaaataa
      N  N  D  T  A  K  S  L  K  V  Q  N  Y  S  F  K  Y  K  N  N
 301 cccatttctaggatttgcaggagctattggttattcaataggcaattcaagaatagaact
      P  F  L  G  F  A  G  A  I  G  Y  S  I  G  N  S  R  I  E  L
 361 agaagtatcacatgaaatatttgatactaaaaacccaggaaacaattatttaaatgactc
      E  V  S  H  E  I  F  D  T  K  N  P  G  N  N  Y  L  N  D  S
 421 tcacaaatattgcgctttatctcatggaagtcacatatgcagtgatggaaatagcggaga
      H  K  Y  C  A  L  S  H  G  S  H  I  C  S  D  G  N  S  G  D
 481 ttggtacactgcaaaaactgataagtttgtacttctgaaaaatgaaggtttacttgacgt
      W  Y  T  A  K  T  D  K  P  V  L  L  K  N  E  G  L  L  D  V
 541 ctcatttatgttaaacgcatgttatgacataacaactgaaaaaatgcctttttcacctta
      S  F  M  L  N  A  C  Y  D  I  T  T  E  K  M  P  F  S  P  Y
 601 tatatgtgcaggtattggtactgatctcatatctatgtttgagacaacacaaaacaaaat
      I  C  A  G  I  G  T  D  L  I  S  M  F  E  T  T  Q  N  K  I
 661 atcttatcaaggaaagttaggtttaaactatactataaactcaagagtttctgtttttgc
      S  Y  Q  G  K  L  G  L  N  Y  T  I  N  S  R  V  S  V  F  A
 721 aggtgggcactttcataaggtaataggtaatgaatttaaaggtattcctactctattacc
      G  G  H  F  H  K  V  I  G  N  E  F  K  G  I  P  T  L  L  P
 781 tgatggatcaaacattaaagtacaacagtctgcaacagtaacattagatgtgtgccattt
      D  G  S  N  I  K  V  Q  Q  S  A  T  V  T  L  D  V  C  H  F
 841 cgggttagagattggaagtagatttttcttttaatacttctattgtacatgttaaaaata
      G  L  E  I  G  S  R  F  F  F  *
 901 gtactagtttgcttctgtggtttataaacgcaagagagaaatagttagtaataaattaga
 961 aagttaaatattagaaaagtcatatgtttttcattgtcattgatactcaactaaaagtag
1021 tataaatgttacttattaataatttacgtagtatattaaatttcccttacaaaagccac
1081 tagtatttttatactaaaagctatactttggcttgtatttaatttgtatttttactactgt
     -35                   -10
1141 caatttactttcactgtttctggtgtaaatatgaattgtaaaaagttttcacaataagt
                         RBS        M  N  C  K  K  V  F  T  I  S
1201 gcattgatatcatccatatacttcctacctaatgtctcatactctaacccagtatatggt
     A  L  I  S  S  I  Y  F  L  P  N  V  S  Y  S  N  P  V  Y  G
1261 aacagtatgtatggtaatttttacatatcaggaaagtacatgccaagtgttcctcatttt
     N  S  M  Y  G  N  F  Y  I  S  G  K  Y  M  P  S  V  P  H  F
1321 ggaatttttcagctgaagaagagaaaaaaaagacaactgtagtatatggcttaaaagaa
     G  I  F  S  A  E  E  E  K  K  K  T  T  V  V  Y  G  L  K  E
1381 aactgggcaggagatgcaatatctagtcaaagtccagatgataatttaccattcgaaat
     N  W  A  G  D  A  I  S  S  Q  S  P  D  D  N  F  T  I  R  N
1441 tactcattcaagtatgcaagcaacaagttttagggtttgcagtagctattggttactcg
     Y  S  F  K  Y  A  S  N  K  P  L  G  F  A  V  A  I  G  Y  S
1501 ataggcagtccaagaatagaagttgagatgtcttatgaagcatttgatgtaaaaaatcaa
     I  G  S  P  R  I  E  V  E  M  S  Y  E  A  P  D  V  K  N  Q
1561 ggtaacaatt
     G  N  N
```

FIG. 2C

```
1     acatgtatacattatagtaacaaatgttaccgtattttattcataagttaagtaaaatct
61    ataccattctctttcactttatcagaagacttttatttatcacaaactcatgacgtatag
121   tgtcacaaataaacacactgcaactgcaatcactacgtaaaactttaactcttcttttc
181   acaactaaaatactaataaaagtaatatagtataaaaaatcttaagtaacTTGACAtaat
                                                         -35
241   attactctgataTAGCATatgtctagtatctctatactaaacgtttatataattGGAGca
                  -10
301   tattaATGAAAGCTATCAAATTCATACTTAATGTCTGCTTACTATTTGCAGCAATATTTT
           M  K  A  I  K  F  I  L  N  V  C  L  L  F  A→ A  I  F  L
361   TAGGGTATTCCTATATTACAAAACAAGGCATATTTCAAACAAAACATCATGATACACCTA
       G  Y  S  Y  I  T  K  Q  G  I  F  Q  T  K  H  H  D  T  P  N
421   ATACTACTATACCAAATGAAGACGGTATTCAATCTAGCTTTAGCTTAATCAATCAAGACG
       T  T  I  P  N  E  D  G  I  Q  S  S  F  S  L  I  N  Q  D  G
481   GTAAAACAGTAACCAGCCAAGATTTCCTAGGGAAACACATGTTAGTTTTGTTTGGATTCT
       K  T  V  T  S  Q  D  F  L  G  K  H  M  L  V  L  F  G  F  S
541   CTGCATGTAAAAGCATTTGCCCTGCAGAATTGGGATTAGTATCTGAAGCACTTGCACAAC
       A  C  K  S  I  C  P  A  E  L  G  L  V  S  E  A  L  A  Q  L
601   TTGGTAATAATGCAGACAAATTACAAGTAATTTTTATTACAATTGATCCAAAAAATGATA
       G  N  N  A  D  K  L  Q  V  I  F  I  T  I  D  P  K  N  D  T
661   CTGTAGAAAAATTAAAAGAATTTCATGAACATTTTGATTCAAGAATTCAAATGTTAACAG
       V  E  K  L  K  E  F  H  E  H  F  D  S  R  I  Q  M  L  T  G
721   GAAATACTGAAGACATTAATCAAATAATTAAAAATTATAAAATATATGTTGGACAAGCAG
       N  T  E  D  I  N  Q  I  I  K  N  Y  K  I  Y  V  G  Q  A  D
781   ATAAAGATCATCAAATTAACCATTCTGCAATAATGTACCTTATTGACAAAAAAGGATCAT
       K  D  H  Q  I  N  H  S  A  I  M  Y  L  I  D  K  K  G  S  Y
841   ATCTTTCACACTTCATTCCAGATTTAAAATCACAAGAAAATCAAGTAGATAAGTTACTAT
       L  S  H  F  I  P  D  L  K  S  Q  E  N  Q  V  D  K  L  L  S
901   CTTTAGTTAAGCAGTATCTGTAAtttaataattaattAAAGagaatagtacacaCTTTtt
       L  V  K  Q  Y  L  *
961   ataaattcatggaatacgttggatgagtaggtttttttagtatttttagtgctaataac
1021  attggcat
```

FIG. 3A

```
1     ggaaatctcatgtaaacgtgaaatactatattctttttaaataccaatacaattgaata
61    caaaaaaacttttacaacttattatgtttatcttaaaaccttattttaagattccttatg
121   tcacaaaataacaaaaatactatttacaaaatacaccacaatttcatcaaataaaaaaa
181   ctatacactttattatactacagtagatataccataaaagattttaagtaacTTGACAta
                                                            -35
241   atattaccttggtaTAGCATatgattcagtattttatattaaatttattatgtattGGA
                    -10
301   GcataaaATGAAAGTTATCAAATTTATACTTAATATCTGTTTATTATTTGCAGCAATTTT
              M  K  V  I  K  F  I  L  N  I  C  L  L  F  A →A  I  F

361   TCTAGGATATTCCTACGTAACAAAACAAGGCATTTTTCAAGTAAGAGATCATAACACTCC
       L  G  Y  S  Y  V  T  K  Q  G  I  F  Q  V  R  D  H  N  T  P

421   CAATACAAATATATCAAATAAAGCCAGCATTACTACTAGTTTTTCGTTAGTAAATCAAGA
       N  T  N  I  S  N  K  A  S  I  T  T  S  F  S  L  V  N  Q  D

481   TGGAAATACAGTAAATAGTCAAGATTTTTTGGGAAAATACATGCTAGTTTTATTTGGATT
       G  N  T  V  N  S  Q  D  F  L  G  K  Y  M  L  V  L  F  G  F

541   TTCTTCATGTAAAAGCATCTGCCCTGCTGAATTAGGAATAGCATCTGAAGTTCTCTCACA
       S  S  C  K  S  I  C  P  A  E  L  G  I  A  S  E  V  L  S  Q

601   GCTTGGTAATGACACAGACAAGTTACAAGTAATTTTCATTACAATTGATCCAACAAATGA
       L  G  N  D  T  D  K  L  Q  V  I  F  I  T  I  D  P  T  N  D

661   TACTGTACAAAAATTAAAAACATTTCATGAACATTTTGATCCTAGAATTCAAATGCTAAC
       T  V  Q  K  L  K  T  F  H  E  H  F  D  P  R  I  Q  M  L  T

721   AGGCAGTGCAGAAGATATTGAAAAAATAATAAAAAATTACAAAATATATGTTGGACAAGC
       G  S  A  E  D  I  E  K  I  I  K  N  Y  K  I  Y  V  G  Q  A

781   AGATAAAGATAATCAAATTGATCACTCTGCCATAATGTACATTATCGATAAAAAAGGAGA
       D  K  D  N  Q  I  D  H  S  A  I  M  Y  I  I  D  K  K  G  E

841   ATACATTTCACACTTTTCTCCAGATTTAAAATCAACAGAAAATCAAGTAGATAAGTTACT
       Y  I  S  H  F  S  P  D  L  K  S  T  E  N  Q  V  D  K  L  L

901   ATCTATAATAAAACAATATCTCTAAtttaataattaattaAAGAGaatagtacacaCTCT
        S  I  I  K  Q  Y  L  *

961   Tatataaattcatggatatatgtgatgggtagatttcttttggtgtttctatcgctaatt
1021  acatta
```

FIG. 3B

SEQUENCE LISTING

<110> University of Florida

<120> Nucleic Acid Vaccines Against Rickettsial Diseases and
Methods of use

<130> UF-167C3

<140>
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<150> 08/953,326
<151> 1997-10-17

<150> 08/733,230
<151> 1996-10-17

<160> 34

<170> PatentIn Ver. 2.0

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atg aat tgc aag aaa att ttt atc aca agt aca cta ata tca tta gtg      48
Met Asn Cys Lys Lys Ile Phe Ile Thr Ser Thr Leu Ile Ser Leu Val
  1               5                  10                  15

tca ttt tta cct ggt gtg tcc ttt tct gat gta ata cag gaa gac agc      96
Ser Phe Leu Pro Gly Val Ser Phe Ser Asp Val Ile Gln Glu Asp Ser
             20                  25                  30

aac cca gca ggc agt gtt tac att agc gca aaa tac atg cca act gca     144
Asn Pro Ala Gly Ser Val Tyr Ile Ser Ala Lys Tyr Met Pro Thr Ala
         35                  40                  45

tca cat ttt ggt aaa atg tca atc aaa gaa gat tca aaa aat act caa     192
Ser His Phe Gly Lys Met Ser Ile Lys Glu Asp Ser Lys Asn Thr Gln
     50                  55                  60

acg gta ttt ggt cta aaa aaa gat tgg gat ggc gtt aaa aca cca tca     240
Thr Val Phe Gly Leu Lys Lys Asp Trp Asp Gly Val Lys Thr Pro Ser
 65                  70                  75                  80

gat tct agc aat act aat tct aca att ttt act gaa aaa gac tat tct     288
```

```
Asp Ser Ser Asn Thr Asn Ser Thr Ile Phe Thr Glu Lys Asp Tyr Ser
                85                  90                  95

ttc aga tat gaa aac aat ccg ttt tta ggt ttc gct gga gca att ggg    336
Phe Arg Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly
            100                 105                 110

tac tca atg aat gga cca aga ata gag ttc gaa gta tcc tat gaa act    384
Tyr Ser Met Asn Gly Pro Arg Ile Glu Phe Glu Val Ser Tyr Glu Thr
        115                 120                 125

ttt gat gta aaa aac cta ggt ggc aac tat aaa aac aac gca cac atg    432
Phe Asp Val Lys Asn Leu Gly Gly Asn Tyr Lys Asn Asn Ala His Met
    130                 135                 140

tac tgt gct tta gat aca gca gca caa aat agc act aat ggc gca gga    480
Tyr Cys Ala Leu Asp Thr Ala Ala Gln Asn Ser Thr Asn Gly Ala Gly
145                 150                 155                 160

tta act aca tct gtt atg gta aaa aac gaa aat tta aca aat ata tca    528
Leu Thr Thr Ser Val Met Val Lys Asn Glu Asn Leu Thr Asn Ile Ser
                165                 170                 175

tta atg tta aat gcg tgt tat gat atc atg ctt gat gga ata cca gtt    576
Leu Met Leu Asn Ala Cys Tyr Asp Ile Met Leu Asp Gly Ile Pro Val
            180                 185                 190

tct cca tat gta tgt gca ggt att ggc act gac tta gtg tca gta att    624
Ser Pro Tyr Val Cys Ala Gly Ile Gly Thr Asp Leu Val Ser Val Ile
        195                 200                 205

aat gct aca aat cct aaa tta tct tat caa gga aag cta ggc ata agt    672
Asn Ala Thr Asn Pro Lys Leu Ser Tyr Gln Gly Lys Leu Gly Ile Ser
    210                 215                 220

tac tca atc aat tct gaa gct tct atc ttt atc ggt gga cat ttc cat    720
Tyr Ser Ile Asn Ser Glu Ala Ser Ile Phe Ile Gly Gly His Phe His
225                 230                 235                 240

aga gtt ata ggt aat gaa ttt aaa gat att gct acc tta aaa ata ttt    768
Arg Val Ile Gly Asn Glu Phe Lys Asp Ile Ala Thr Leu Lys Ile Phe
                245                 250                 255

act tca aaa aca gga ata tct aat cct ggc ttt gca tca gca aca ctt    816
Thr Ser Lys Thr Gly Ile Ser Asn Pro Gly Phe Ala Ser Ala Thr Leu
            260                 265                 270

gat gtt tgt cac ttt ggt ata gaa att gga gga agg ttt gta ttt taa    864
Asp Val Cys His Phe Gly Ile Glu Ile Gly Gly Arg Phe Val Phe
        275                 280                 285
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Met Asn Cys Lys Lys Ile Phe Ile Thr Ser Thr Leu Ile Ser Leu Val
 1               5                  10                  15

Ser Phe Leu Pro Gly Val Ser Phe Ser Asp Val Ile Gln Glu Asp Ser
            20                  25                  30

Asn Pro Ala Gly Ser Val Tyr Ile Ser Ala Lys Tyr Met Pro Thr Ala
        35                  40                  45

Ser His Phe Gly Lys Met Ser Ile Lys Glu Asp Ser Lys Asn Thr Gln
    50                  55                  60

Thr Val Phe Gly Leu Lys Lys Asp Trp Asp Gly Val Lys Thr Pro Ser
65                  70                  75                  80

Asp Ser Ser Asn Thr Asn Ser Thr Ile Phe Thr Glu Lys Asp Tyr Ser
                85                  90                  95

Phe Arg Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly
            100                 105                 110

Tyr Ser Met Asn Gly Pro Arg Ile Glu Phe Glu Val Ser Tyr Glu Thr
        115                 120                 125

Phe Asp Val Lys Asn Leu Gly Gly Asn Tyr Lys Asn Asn Ala His Met
    130                 135                 140

Tyr Cys Ala Leu Asp Thr Ala Ala Gln Asn Ser Thr Asn Gly Ala Gly
145                 150                 155                 160

Leu Thr Thr Ser Val Met Val Lys Asn Glu Asn Leu Thr Asn Ile Ser
                165                 170                 175

Leu Met Leu Asn Ala Cys Tyr Asp Ile Met Leu Asp Gly Ile Pro Val
            180                 185                 190

Ser Pro Tyr Val Cys Ala Gly Ile Gly Thr Asp Leu Val Ser Val Ile
        195                 200                 205

Asn Ala Thr Asn Pro Lys Leu Ser Tyr Gln Gly Lys Leu Gly Ile Ser
    210                 215                 220

Tyr Ser Ile Asn Ser Glu Ala Ser Ile Phe Ile Gly Gly His Phe His
225                 230                 235                 240

Arg Val Ile Gly Asn Glu Phe Lys Asp Ile Ala Thr Leu Lys Ile Phe
                245                 250                 255

Thr Ser Lys Thr Gly Ile Ser Asn Pro Gly Phe Ala Ser Ala Thr Leu
            260                 265                 270

Asp Val Cys His Phe Gly Ile Glu Ile Gly Gly Arg Phe Val Phe
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275 280 285

<210> 3
<211> 842
<212> DNA
<213> Ehrlichia chaffeensis

<220>
<221> CDS
<222> (1)..(840)

<400> 3
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Met Asn Tyr Lys Lys Ser Phe Ile Thr Ala Ile Asp Ile Ile Asn Ile
  1               5                  10                  15

ctt ctc tta cct gga gta tca ttt tcc gac cca agg cag gta gtg gtc      96
Leu Leu Leu Pro Gly Val Ser Phe Ser Asp Pro Arg Gln Val Val Val
             20                  25                  30

att aac ggt aat ttc tac atc agt gga aaa tac gat gcc aag gct tcg     144
Ile Asn Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Asp Ala Lys Ala Ser
         35                  40                  45

cat ttt gga gta ttc tct gct aag gaa gaa aga aat aca aca gtt gga     192
His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly
     50                  55                  60

gtg ttt gga ctg aag caa aat tgg gac gga agc gca ata tcc aac tcc     240
Val Phe Gly Leu Lys Gln Asn Trp Asp Gly Ser Ala Ile Ser Asn Ser
 65                  70                  75                  80

tcc cca aac gat gta ttc act gtc tca aat tat tca ttt aaa tat gaa     288
Ser Pro Asn Asp Val Phe Thr Val Ser Asn Tyr Ser Phe Lys Tyr Glu
                 85                  90                  95

aac aac ccg ttt tta ggt ttt gca gga gct att ggt tac tca atg gat     336
Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Asp
            100                 105                 110

ggt cca aga ata gag ctt gaa gta tct tat gaa aca ttt gat gta aaa     384
Gly Pro Arg Ile Glu Leu Glu Val Ser Tyr Glu Thr Phe Asp Val Lys
        115                 120                 125

aat caa ggt aac aat tat aag aat gaa gca cat aga tat tgt gct cta     432
Asn Gln Gly Asn Asn Tyr Lys Asn Glu Ala His Arg Tyr Cys Ala Leu
    130                 135                 140

tcc cat aac tca gca gca gac atg agt agt gca agt aat aat ttt gtc     480
Ser His Asn Ser Ala Ala Asp Met Ser Ser Ala Ser Asn Asn Phe Val
145                 150                 155                 160

ttt cta aaa aat gaa gga tta ctt gac ata tca ttt atg ctg aac gca     528
Phe Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala
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                165                     170                     175

tgc tat gac gta gta ggc gaa ggc ata cct ttt tct cct tat ata tgc      576
Cys Tyr Asp Val Val Gly Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys
            180                     185                     190

gca ggt atc ggt act gat tta gta tcc atg ttt gaa gct aca aat cct      624
Ala Gly Ile Gly Thr Asp Leu Val Ser Met Phe Glu Ala Thr Asn Pro
        195                     200                     205

aaa att tct tac caa gga aag tta ggt tta agc tac tct ata agc cca      672
Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro
    210                     215                     220

gaa gct tct gtg ttt att ggt ggg cac ttt cat aag gta ata ggg aac      720
Glu Ala Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn
225                     230                     235                     240

gaa ttt aga gat att cct act ata ata cct act gga tca aca ctt gca      768
Glu Phe Arg Asp Ile Pro Thr Ile Ile Pro Thr Gly Ser Thr Leu Ala
                245                     250                     255

gga aaa gga aac tac cct gca ata gta ata ctg gat gta tgc cac ttt      816
Gly Lys Gly Asn Tyr Pro Ala Ile Val Ile Leu Asp Val Cys His Phe
            260                     265                     270

gga ata gaa atg gga gga agg ttt aa                                   842
Gly Ile Glu Met Gly Gly Arg Phe
        275                     280


&lt;210&gt; 4
&lt;211&gt; 280
&lt;212&gt; PRT
&lt;213&gt; Ehrlichia chaffeensis

&lt;400&gt; 4
Met Asn Tyr Lys Lys Ser Phe Ile Thr Ala Ile Asp Ile Ile Asn Ile
  1               5                  10                  15

Leu Leu Leu Pro Gly Val Ser Phe Ser Asp Pro Arg Gln Val Val Val
            20                  25                  30

Ile Asn Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Asp Ala Lys Ala Ser
        35                  40                  45

His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly
    50                  55                  60

Val Phe Gly Leu Lys Gln Asn Trp Asp Gly Ser Ala Ile Ser Asn Ser
65                  70                  75                  80

Ser Pro Asn Asp Val Phe Thr Val Ser Asn Tyr Ser Phe Lys Tyr Glu
                85                  90                  95
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Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Asp
            100   105   110

Gly Pro Arg Ile Glu Leu Glu Val Ser Tyr Glu Thr Phe Asp Val Lys
        115   120   125

Asn Gln Gly Asn Asn Tyr Lys Asn Glu Ala His Arg Tyr Cys Ala Leu
    130   135   140

Ser His Asn Ser Ala Ala Asp Met Ser Ser Ala Ser Asn Asn Phe Val
145   150   155   160

Phe Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala
                165   170   175

Cys Tyr Asp Val Val Gly Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys
            180   185   190

Ala Gly Ile Gly Thr Asp Leu Val Ser Met Phe Glu Ala Thr Asn Pro
        195   200   205

Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro
    210   215   220

Glu Ala Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn
225   230   235   240

Glu Phe Arg Asp Ile Pro Thr Ile Ile Pro Thr Gly Ser Thr Leu Ala
                245   250   255

Gly Lys Gly Asn Tyr Pro Ala Ile Val Ile Leu Asp Val Cys His Phe
            260   265   270

Gly Ile Glu Met Gly Gly Arg Phe
        275   280

<210> 5
<211> 849
<212> DNA
<213> Anaplasma marginale

<220>
<221> CDS
<222> (1)..(846)

<400> 5

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Met Asn Tyr Arg Glu Leu Phe Thr Gly Gly Leu Ser Ala Ala Thr Val
 1               5                  10                  15

tgc gcc tgc tcc cta ctt gtt agt ggg gcc gta gtg gca tct ccc atg     96
Cys Ala Cys Ser Leu Leu Val Ser Gly Ala Val Val Ala Ser Pro Met
            20                  25                  30

agt cac gaa gtg gct tct gaa ggg gga gta atg gga ggt agc ttt tac     144
Ser His Glu Val Ala Ser Glu Gly Gly Val Met Gly Gly Ser Phe Tyr
        35                  40                  45

gtg ggt gcg gcc tac agc cca gca ttt cct tct gtt acc tcg ttc gac     192
Val Gly Ala Ala Tyr Ser Pro Ala Phe Pro Ser Val Thr Ser Phe Asp
    50                  55                  60

atg cgt gag tca agc aaa gag acc tca tac gtt aga ggc tat gac aag     240
Met Arg Glu Ser Ser Lys Glu Thr Ser Tyr Val Arg Gly Tyr Asp Lys
65                  70                  75                  80

agc att gca acg att gat gtg agt gtg cca gca aac ttt tcc aaa tct     288
Ser Ile Ala Thr Ile Asp Val Ser Val Pro Ala Asn Phe Ser Lys Ser
                85                  90                  95

ggc tac act ttt gcc ttc tct aaa aac tta atc acg tct ttc gac ggc     336
Gly Tyr Thr Phe Ala Phe Ser Lys Asn Leu Ile Thr Ser Phe Asp Gly
            100                 105                 110

gct gtg gga tat tct ctg gga gga gcc aga gtg gaa ttg gaa gcg agc     384
Ala Val Gly Tyr Ser Leu Gly Gly Ala Arg Val Glu Leu Glu Ala Ser
        115                 120                 125

tac aga agg ttt gct act ttg gcg gac ggg cag tac gca aaa agt ggt     432
Tyr Arg Arg Phe Ala Thr Leu Ala Asp Gly Gln Tyr Ala Lys Ser Gly
    130                 135                 140

gcg gaa tct ctg gca gct att acc cgc gac gct aac att act gag acc     480
Ala Glu Ser Leu Ala Ala Ile Thr Arg Asp Ala Asn Ile Thr Glu Thr
145                 150                 155                 160

aat tac ttc gta gtc aaa att gat gaa atc aca aac acc tca gtc atg     528
Asn Tyr Phe Val Val Lys Ile Asp Glu Ile Thr Asn Thr Ser Val Met
                165                 170                 175

tta aat ggc tgc tat gac gtg ctg cac aca gat tta cct gtg tcc ccg     576
Leu Asn Gly Cys Tyr Asp Val Leu His Thr Asp Leu Pro Val Ser Pro
            180                 185                 190

tat gta tgt gcc ggg ata ggc gca agc ttt gtt gac atc tct aag caa     624
Tyr Val Cys Ala Gly Ile Gly Ala Ser Phe Val Asp Ile Ser Lys Gln
        195                 200                 205

gta acc aca aag ctg gcc tac agg ggc aag gtt ggg att agc tac cag     672
Val Thr Thr Lys Leu Ala Tyr Arg Gly Lys Val Gly Ile Ser Tyr Gln
    210                 215                 220
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ttt act ccg gaa ata tcc ttg gtg gca ggt ggg ttc tac cac ggg cta 720
Phe Thr Pro Glu Ile Ser Leu Val Ala Gly Gly Phe Tyr His Gly Leu
225 230 235 240

ttt gat gag tct tac aag gac att ccc gca cac aac agt gta aag ttc 768
Phe Asp Glu Ser Tyr Lys Asp Ile Pro Ala His Asn Ser Val Lys Phe
245 250 255

tct gga gaa gca aaa gcc tca gtc aaa gcg cat att gct gac tac ggc 816
Ser Gly Glu Ala Lys Ala Ser Val Lys Ala His Ile Ala Asp Tyr Gly
260 265 270

ttt aac ctt gga gca aga ttc ctg ttc agc taa 849
Phe Asn Leu Gly Ala Arg Phe Leu Phe Ser
275 280

<210> 6
<211> 282
<212> PRT
<213> Anaplasma marginale

<400> 6
Met Asn Tyr Arg Glu Leu Phe Thr Gly Gly Leu Ser Ala Ala Thr Val
1 5 10 15

Cys Ala Cys Ser Leu Leu Val Ser Gly Ala Val Val Ala Ser Pro Met
20 25 30

Ser His Glu Val Ala Ser Glu Gly Gly Val Met Gly Gly Ser Phe Tyr
35 40 45

Val Gly Ala Ala Tyr Ser Pro Ala Phe Pro Ser Val Thr Ser Phe Asp
50 55 60

Met Arg Glu Ser Ser Lys Glu Thr Ser Tyr Val Arg Gly Tyr Asp Lys
65 70 75 80

Ser Ile Ala Thr Ile Asp Val Ser Val Pro Ala Asn Phe Ser Lys Ser
85 90 95

Gly Tyr Thr Phe Ala Phe Ser Lys Asn Leu Ile Thr Ser Phe Asp Gly
100 105 110

Ala Val Gly Tyr Ser Leu Gly Gly Ala Arg Val Glu Leu Glu Ala Ser
115 120 125

Tyr Arg Arg Phe Ala Thr Leu Ala Asp Gly Gln Tyr Ala Lys Ser Gly
130 135 140

Ala Glu Ser Leu Ala Ala Ile Thr Arg Asp Ala Asn Ile Thr Glu Thr
145 150 155 160

Asn Tyr Phe Val Val Lys Ile Asp Glu Ile Thr Asn Thr Ser Val Met
165 170 175

Leu Asn Gly Cys Tyr Asp Val Leu His Thr Asp Leu Pro Val Ser Pro
180 185 190

Tyr Val Cys Ala Gly Ile Gly Ala Ser Phe Val Asp Ile Ser Lys Gln
195 200 205

Val Thr Thr Lys Leu Ala Tyr Arg Gly Lys Val Gly Ile Ser Tyr Gln
210 215 220

Phe Thr Pro Glu Ile Ser Leu Val Ala Gly Gly Phe Tyr His Gly Leu
225 230 235 240

Phe Asp Glu Ser Tyr Lys Asp Ile Pro Ala His Asn Ser Val Lys Phe
245 250 255

Ser Gly Glu Ala Lys Ala Ser Val Lys Ala His Ile Ala Asp Tyr Gly
260 265 270

Phe Asn Leu Gly Ala Arg Phe Leu Phe Ser
275 280

<210> 7
<211> 132
<212> DNA
<213> Ehrlichia chaffeensis

<400> 7
ggaatgaatt cagggacatt tctactctta aagcgtttgc tacaccatca tctgcagcta 60

ctccagactt agcaacagta acactgagtg tgtgtcactt tggagtagaa cttggaggaa 120

gatttaactt ct 132

<210> 8
<211> 861
<212> DNA
<213> Ehrlichia chaffeensis

<400> 8
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ctggaatatc actttctgat ccagtacagg atgacaacat tagtggtaat ttctacatca 120

gtggaaagta tatgccaagc gcttcgcatt ttggagtttt ttctgccaag gaagaaagaa 180

atacaacagt tggagtattt ggaatagagc aagattggga tagatgtgta atatctagaa 240

ccactttaag cgatatattc accgttccaa attattcatt taagtatgaa aataatctat 300

tttcaggatt tgcaggagct attggctact caatggatgg cccaagaata gagcttgaag 360

tatcttatga agcattcgat gttaaaaatc aaggtaacaa ttataagaac gaagcacata 420

gatattatgc tctgtcccat cttctcggca cagagacaca gatagatggt gcaggcagtg 480

cgtctgtctt tctaataaat gaaggactac ttgataaatc atttatgctg aacgcatgtt 540

atgatgtaat aagtgaaggc ataccttttt ctccttatat atgtgcaggt attggtattg 600

atttagtatc catgtttgaa gctataaatc ctaaaatttc ttatcaagga aaattaggct 660

taagttaccc tataagccca gaagcttctg tgtttattgg tggacatttt cataaggtga 720

taggaaacga atttagagat attcctacta tgatacctag tgaatcagcg cttgcaggaa 780

aaggaaacta ccctgcaata gtaacactgg acgtgttcta ctttggcata gaacttggag 840

gaaggtttaa cttccaactt t 861

<210> 9
<211> 837
<212> DNA
<213> Ehrlichia chaffeensis

<400> 9
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ctggaatatc attttctgat ccagtgcaag gtgacaatat tagtggtaat ttctatgtta 120

gtggcaagta tatgccaagt gcttcgcatt ttggcatgtt ttctgccaaa gaagaaaaaa 180

atcctactgt tgcattgtat ggcttaaaac aagattggga agggattagc tcatcaagtc 240

acaatgataa tcatttcaat aacaagggtt attcatttaa atatgaaaat aacccatttt 300

tagggtttgc aggagctatt ggttattcaa tgggtggtcc aagagtagag tttgaagtgt 360

cctatgaaac atttgacgtt aaaaatcagg gtaataacta taaaaatgat gctcacagat 420

actgtgcttt aggtcaacaa gacaacagcg gaatacctaa aactagtaaa tacgtactgt 480

taaaaagcga aggattgctt gacatatcat ttatgctaaa tgcatgctat gatataataa 540

acgagagcat acctttgtct ccttacatat gtgcaggtgt tggtactgat ttaatatcca 600

tgtttgaagc tacaaatcct aaaatttctt accaagggaa gttaggtcta agttactcta 660

taaacccaga agcttctgta tttattggtg gacattttca taaggtgata ggaaacgaat 720

ttagggacat tcctactctg aaagcatttg ttacgtcatc agctactcca gatctagcaa 780

tagtaacact aagtgtatgt cattttggaa tagaacttgg aggaaggttt aacttct 837

<210> 10
<211> 843
<212> DNA

<213> Ehrlichia chaffeensis

<400> 10
atatgaattg caaaaaattt tttataacaa ctacattagt atcgctaatg tccttcttac 60

ctggaatatc attttctgat gcagtacaga acgacaatgt tggtggtaat ttctatatca 120

gtgggaaata tgtaccaagt gtttcacatt ttggcgtatt ctctgctaaa caggaaagaa 180

atacaacaat cggagtattt ggattaaagc aagattggga tggcagcaca atatctaaaa 240

attctccaga aaatacattt aacgttccaa attattcatt taaatatgaa aataatccat 300

ttctaggttt tgcaggagct gttggttatt taatgaatgg tccaagaata gagttagaaa 360

tgtcctatga aacatttgat gtgaaaaacc agggtaataa ctataagaac gatgctcaca 420

aatattatgc tttaacccat aacagtgggg gaaagctaag caatgcaggt gataagtttg 480

tttttctaaa aaatgaagga ctacttgata tatcacttat gttgaatgca tgctatgatg 540

taataagtga aggaatacct ttctctcctt acatatgtgc aggtgttggt actgatttaa 600

tatccatgtt tgaagctata aaccctaaaa tttcttatca aggaaagtta ggtttgagtt 660

actccataag cccagaagct tctgtttttg ttggtggaca ttttcataag gtgataggga 720

atgaattcag agatattcct gctatgatac ccagtacctc aactctcaca ggtaatcact 780

ttactatagt aacactaagt gtatgccact ttggagtgga acttggagga aggtttaact 840

ttt 843

<210> 11
<211> 830
<212> DNA
<213> Ehrlichia chaffeensis

<400> 11
atatgaatta caaaaaagtt ttcataacaa gtgcattgat atcattaata tcttctctac 60

ctggagtatc attttccgac ccagcaggta gtggtattaa cggtaatttc tacatcagtg 120

gaaaatacat gccaagtgct tcgcattttg gagtattctc tgctaaggaa gaaagaaata 180

caacagttgg agtgtttgga ctgaagcaaa attgggacgg aagcgcaata tccaactcct 240

ccccaaacga tgtattcact gtctcaaatt attcatttaa atatgaaaac aacccgtttt 300

taggttttgc aggagctatt ggttactcaa tggatggtcc aagaatagag cttgaagtat 360

cttatgaaac atttgatgta aaaaatcaag gtaacaatta taagaatgaa gcacatagat 420

attgtgctct atcccataac tcagcagcag acatgagtag tgcaagtaat aattttgtct 480

ttctaaaaaa tgaaggatta cttgacatat catttatgct gaacgcatgc tatgacgtag 540

taggcgaagg catacctttt tctccttata tatgcgcagg tatcggtact gatttagtat 600

ccatgtttga agctacaaat cctaaaattt cttaccaagg aaagttaggt ttaagctact 660

ctataagccc agaagcttct gtgtttattg gtgggcactt tcataaggta atagggaacg 720

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accctgcaat agtaatactg gatgtatgcc actttggaat agaaatggga 830

<210> 12
<211> 864
<212> DNA
<213> Ehrlichia canis

<400> 12
atatgaaata taaaaaaact tttacagtaa ctgcattagt attattaact tcctttacac 60

attttatacc tttttatagt ccagcacgtg ccagtacaat tcacaacttc tacattagtg 120

gaaaatatat gccaacagcg tcacattttg gaatttttc agctaaagaa gaacaaagtt 180

ttactaaggt attagttggg ttagatcaac gattatcaca taatattata aacaataatg 240

atacagcaaa gagtcttaag gttcaaaatt attcatttaa atacaaaaat aacccatttc 300

taggatttgc aggagctatt ggttattcaa taggcaattc aagaatagaa ctagaagtat 360

cacatgaaat atttgatact aaaaacccag gaaacaatta tttaaatgac tctcacaaat 420

attgcgcttt atctcatgga agtcacatat gcagtgatgg aaatagcgga gattggtaca 480

ctgcaaaaac tgataagttt gtacttctga aaaatgaagg tttacttgac gtctcattta 540

tgttaaacgc atgttatgac ataacaactg aaaaaatgcc tttttcacct tatatatgtg 600

caggtattgg tactgatctc atatctatgt ttgagacaac acaaaacaaa atatcttatc 660

aaggaaagtt aggtttaaac tatactataa actcaagagt ttctgttttt gcaggtgggc 720

actttcataa ggtaataggt aatgaattta aaggtattcc tactctatta cctgatggat 780

caaacattaa agtacaacag tctgcaacag taacattaga tgtgtgccat ttcgggttag 840

agattggaag tagatttttc tttt 864

<210> 13
<211> 399
<212> DNA
<213> Ehrlichia canis

<400> 13
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ctaatgtctc atactctaac ccagtatatg gtaacagtat gtatggtaat ttttacatat 120

caggaaagta catgccaagt gttcctcatt ttggaatttt ttcagctgaa gaagagaaaa 180

aaaagacaac tgtagtatat ggcttaaaag aaaactgggc aggagatgca atatctagtc 240

aaagtccaga tgataatttt accattcgaa attactcatt caagtatgca agcaacaagt 300

ttttagggtt tgcagtagct attggttact cgataggcag tccaagaata gaagttgaga 360

tgtcttatga agcatttgat gtaaaaaatc aaggtaaca 399

<210> 14
<211> 43
<212> PRT
<213> Ehrlichia chaffeensis

<400> 14
Asn Glu Phe Arg Asp Ile Ser Thr Leu Lys Ala Phe Ala Thr Pro Ser
1 5 10 15

Ser Ala Ala Thr Pro Asp Leu Ala Thr Val Thr Leu Ser Val Cys His
20 25 30

Phe Gly Val Glu Leu Gly Gly Arg Phe Asn Phe
35 40

<210> 15
<211> 286
<212> PRT
<213> Ehrlichia chaffeensis

<400> 15
Met Asn Cys Glu Lys Phe Phe Ile Thr Thr Ala Leu Thr Leu Leu Met
1 5 10 15

Ser Phe Leu Pro Gly Ile Ser Leu Ser Asp Pro Val Gln Asp Asp Asn
20 25 30

Ile Ser Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Ala Ser
35 40 45

His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly
50 55 60

Val Phe Gly Ile Glu Gln Asp Trp Asp Arg Cys Val Ile Ser Arg Thr
65 70 75 80

Thr Leu Ser Asp Ile Phe Thr Val Pro Asn Tyr Ser Phe Lys Tyr Glu
85 90 95

Asn Asn Leu Phe Ser Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Asp
100 105 110

Gly Pro Arg Ile Glu Leu Glu Val Ser Tyr Glu Ala Phe Asp Val Lys
115 120 125

Asn Gln Gly Asn Asn Tyr Lys Asn Glu Ala His Arg Tyr Tyr Ala Leu
130 135 140

Ser His Leu Leu Gly Thr Glu Thr Gln Ile Asp Gly Ala Gly Ser Ala
145 150 155 160

Ser Val Phe Leu Ile Asn Glu Gly Leu Leu Asp Lys Ser Phe Met Leu
165 170 175

Asn Ala Cys Tyr Asp Val Ile Ser Glu Gly Ile Pro Phe Ser Pro Tyr
180 185 190

Ile Cys Ala Gly Ile Gly Ile Asp Leu Val Ser Met Phe Glu Ala Ile
195 200 205

Asn Pro Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Pro Ile
210 215 220

Ser Pro Glu Ala Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile
225 230 235 240

Gly Asn Glu Phe Arg Asp Ile Pro Thr Met Ile Pro Ser Glu Ser Ala
245 250 255

Leu Ala Gly Lys Gly Asn Tyr Pro Ala Ile Val Thr Leu Asp Val Phe
260 265 270

Tyr Phe Gly Ile Glu Leu Gly Gly Arg Phe Asn Phe Gln Leu
275 280 285

<210> 16
<211> 278
<212> PRT
<213> Ehrlichia chaffeensis

<400> 16
Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Ala Leu Val Ser Leu Met
1 5 10 15

Ser Phe Leu Pro Gly Ile Ser Phe Ser Asp Pro Val Gln Gly Asp Asn
20 25 30

Ile Ser Gly Asn Phe Tyr Val Ser Gly Lys Tyr Met Pro Ser Ala Ser
35 40 45

His Phe Gly Met Phe Ser Ala Lys Glu Glu Lys Asn Pro Thr Val Ala
50 55 60

Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile Ser Ser Ser Ser His
65   70   75   80

Asn Asp Asn His Phe Asn Asn Lys Gly Tyr Ser Phe Lys Tyr Glu Asn
                85   90   95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly
            100   105   110

Pro Arg Val Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn
        115   120   125

Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Gly
    130   135   140

Gln Gln Asp Asn Ser Gly Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu
145   150   155   160

Lys Ser Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr
                165   170   175

Asp Ile Ile Asn Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly
            180   185   190

Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile
        195   200   205

Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala
    210   215   220

Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe
225   230   235   240

Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr Pro
                245   250   255

Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu
            260   265   270

Gly Gly Arg Phe Asn Phe
        275

<210> 17
<211> 280
<212> PRT
<213> Ehrlichia chaffeensis

<400> 17
Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Thr Leu Val Ser Leu Met
  1   5   10   15

Ser Phe Leu Pro Gly Ile Ser Phe Ser Asp Ala Val Gln Asn Asp Asn
            20   25   30

Val Gly Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser Val Ser
35 40 45

His Phe Gly Val Phe Ser Ala Lys Gln Glu Arg Asn Thr Thr Ile Gly
50 55 60

Val Phe Gly Leu Lys Gln Asp Trp Asp Gly Ser Thr Ile Ser Lys Asn
65 70 75 80

Ser Pro Glu Asn Thr Phe Asn Val Pro Asn Tyr Ser Phe Lys Tyr Glu
85 90 95

Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala Val Gly Tyr Leu Met Asn
100 105 110

Gly Pro Arg Ile Glu Leu Glu Met Ser Tyr Glu Thr Phe Asp Val Lys
115 120 125

Asn Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Lys Tyr Tyr Ala Leu
130 135 140

Thr His Asn Ser Gly Gly Lys Leu Ser Asn Ala Gly Asp Lys Phe Val
145 150 155 160

Phe Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Leu Met Leu Asn Ala
165 170 175

Cys Tyr Asp Val Ile Ser Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys
180 185 190

Ala Gly Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Ile Asn Pro
195 200 205

Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro
210 215 220

Glu Ala Ser Val Phe Val Gly Gly His Phe His Lys Val Ile Gly Asn
225 230 235 240

Glu Phe Arg Asp Ile Pro Ala Met Ile Pro Ser Thr Ser Thr Leu Thr
245 250 255

Gly Asn His Phe Thr Ile Val Thr Leu Ser Val Cys His Phe Gly Val
260 265 270

Glu Leu Gly Gly Arg Phe Asn Phe
275 280

<210> 18
<211> 276
<212> PRT
<213> Ehrlichia chaffeensis

<400> 18

Met Asn Tyr Lys Lys Val Phe Ile Thr Ser Ala Leu Ile Ser Leu Ile
1 5 10 15

Ser Ser Leu Pro Gly Val Ser Phe Ser Asp Pro Ala Gly Ser Gly Ile
20 25 30

Asn Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Ala Ser His
35 40 45

Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly Val
50 55 60

Phe Gly Leu Lys Gln Asn Trp Asp Gly Ser Ala Ile Ser Asn Ser Ser
65 70 75 80

Pro Asn Asp Val Phe Thr Val Ser Asn Tyr Ser Phe Lys Tyr Glu Asn
85 90 95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Asp Gly
100 105 110

Pro Arg Ile Glu Leu Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn
115 120 125

Gln Gly Asn Asn Tyr Lys Asn Glu Ala His Arg Tyr Cys Ala Leu Ser
130 135 140

His Asn Ser Ala Ala Asp Met Ser Ser Ala Ser Asn Asn Phe Val Phe
145 150 155 160

Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys
165 170 175

Tyr Asp Val Val Gly Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala
180 185 190

Gly Ile Gly Thr Asp Leu Val Ser Met Phe Glu Ala Thr Asn Pro Lys
195 200 205

Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro Glu
210 215 220

Ala Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu
225 230 235 240

Phe Arg Asp Ile Pro Thr Ile Ile Pro Thr Gly Ser Thr Leu Ala Gly
245 250 255

Lys Gly Asn Tyr Pro Ala Ile Val Ile Leu Asp Val Cys His Phe Gly
260 265 270

Ile Glu Met Gly
275

<210> 19
<211> 287
<212> PRT
<213> Ehrlichia canis

<400> 19
Met Lys Tyr Lys Lys Thr Phe Thr Val Thr Ala Leu Val Leu Leu Thr
1 5 10 15

Ser Phe Thr His Phe Ile Pro Phe Tyr Ser Pro Ala Arg Ala Ser Thr
20 25 30

Ile His Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Thr Ala Ser His
35 40 45

Phe Gly Ile Phe Ser Ala Lys Glu Glu Gln Ser Phe Thr Lys Val Leu
50 55 60

Val Gly Leu Asp Gln Arg Leu Ser His Asn Ile Ile Asn Asn Asn Asp
65 70 75 80

Thr Ala Lys Ser Leu Lys Val Gln Asn Tyr Ser Phe Lys Tyr Lys Asn
85 90 95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Ile Gly Asn
100 105 110

Ser Arg Ile Glu Leu Glu Val Ser His Glu Ile Phe Asp Thr Lys Asn
115 120 125

Pro Gly Asn Asn Tyr Leu Asn Asp Ser His Lys Tyr Cys Ala Leu Ser
130 135 140

His Gly Ser His Ile Cys Ser Asp Gly Asn Ser Gly Asp Trp Tyr Thr
145 150 155 160

Ala Lys Thr Asp Lys Phe Val Leu Leu Lys Asn Glu Gly Leu Leu Asp
165 170 175

Val Ser Phe Met Leu Asn Ala Cys Tyr Asp Ile Thr Thr Glu Lys Met
180 185 190

Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp Leu Ile Ser
195 200 205

Met Phe Glu Thr Thr Gln Asn Lys Ile Ser Tyr Gln Gly Lys Leu Gly
210 215 220

Leu Asn Tyr Thr Ile Asn Ser Arg Val Ser Val Phe Ala Gly Gly His
225 230 235 240

Phe His Lys Val Ile Gly Asn Glu Phe Lys Gly Ile Pro Thr Leu Leu
245 250 255

Pro Asp Gly Ser Asn Ile Lys Val Gln Gln Ser Ala Thr Val Thr Leu
260 265 270

Asp Val Cys His Phe Gly Leu Glu Ile Gly Ser Arg Phe Phe Phe
275 280 285

<210> 20
<211> 133
<212> PRT
<213> Ehrlichia canis

<400> 20
Met Asn Cys Lys Lys Val Phe Thr Ile Ser Ala Leu Ile Ser Ser Ile
1 5 10 15

Tyr Phe Leu Pro Asn Val Ser Tyr Ser Asn Pro Val Tyr Gly Asn Ser
20 25 30

Met Tyr Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Val Pro
35 40 45

His Phe Gly Ile Phe Ser Ala Glu Glu Glu Lys Lys Lys Thr Thr Val
50 55 60

Val Tyr Gly Leu Lys Glu Asn Trp Ala Gly Asp Ala Ile Ser Ser Gln
65 70 75 80

Ser Pro Asp Asp Asn Phe Thr Ile Arg Asn Tyr Ser Phe Lys Tyr Ala
85 90 95

Ser Asn Lys Phe Leu Gly Phe Ala Val Ala Ile Gly Tyr Ser Ile Gly
100 105 110

Ser Pro Arg Ile Glu Val Glu Met Ser Tyr Glu Ala Phe Asp Val Lys
115 120 125

Asn Gln Gly Asn Asn
130

<210> 21
<211> 686
<212> DNA
<213> Ehrlichia canis

<400> 21
atgaaagcta tcaaattcat acttaatgtc tgcttactat ttgcagcaat atttttaggg 60

tattcctata ttacaaaaca aggcatattt caaacaaaac atcatgatac acctaatact 120

actataccaa atgaagacgg tattcaatct agctttagct taatcaatca agacggtaaa 180

acagtaacca gccaagattt cctagggaaa cacatgttag ttttgtttgg attctctgca 240

tgtaaaagca tttgccctgc agaattggga ttagtatctg aagcacttgc acaacttggt 300

aataatgcag acaaattaca agtaattttt attacaattg atccaaaaaa tgatactgta 360

gaaaaattaa aagaatttca tgaacatttt gattcaagaa ttcaaatgtt aacaggaaat 420

actgaagaca ttaatcaaat aattaaaaat tataaaatat atgttggaca agcagataaa 480

gatcatcaaa ttaaccattc tgcaataatg taccttattg acaaaaaagg atcatatctt 540

tcacacttca ttccagattt aaaatcacaa gaaaatcaag tagataagtt actatcttta 600

gttaagcagt atctgtaaat aaattcatgg aatacgttgg atgagtaggt tttttttagt 660

atttttagtg ctaataacat tggcat 686

<210> 22
<211> 618
<212> DNA
<213> Ehrlichia chaffeensis

<400> 22
atgaaagtta tcaaatttat acttaatatc tgtttattat ttgcagcaat ttttctagga 60

tattcctacg taacaaaaca aggcattttt caagtaagag atcataacac tcccaataca 120

aatatatcaa ataaagccag cattactact agtttttcgt tagtaaatca agatggaaat 180

acagtaaata gtcaagattt tttgggaaaa tacatgctag ttttatttgg attttcttca 240

tgtaaaagca tctgccctgc tgaattagga atagcatctg aagttctctc acagcttggt 300

aatgacacag acaagttaca agtaattttc attacaattg atccaacaaa tgatactgta 360

caaaaattaa aaacatttca tgaacatttt gatcctagaa ttcaaatgct aacaggcagt 420

gcagaagata ttgaaaaaat aataaaaaat tacaaaatat atgttggaca agcagataaa 480

gataatcaaa ttgatcactc tgccataatg tacattatcg ataaaaaagg agaatacatt 540

tcacactttt ctccagattt aaaatcaaca gaaaatcaag tagataagtt actatctata 600

ataaaacaat atctctaa 618

<210> 23
<211> 205
<212> PRT
<213> Ehrlichia canis

<400> 23
Met Lys Ala Ile Lys Phe Ile Leu Asn Val Cys Leu Leu Phe Ala Ala
1 5 10 15

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Ile Phe Leu Gly Tyr Ser Tyr Ile Thr Lys Gln Gly Ile Phe Gln Thr
            20                  25                  30

Lys His His Asp Thr Pro Asn Thr Thr Ile Pro Asn Glu Asp Gly Ile
        35                  40                  45

Gln Ser Ser Phe Ser Leu Ile Asn Gln Asp Gly Lys Thr Val Thr Ser
    50                  55                  60

Gln Asp Phe Leu Gly Lys His Met Leu Val Leu Phe Gly Phe Ser Ala
65                  70                  75                      80

Cys Lys Ser Ile Cys Pro Ala Glu Leu Gly Leu Val Ser Glu Ala Leu
                85                  90                  95

Ala Gln Leu Gly Asn Asn Ala Asp Lys Leu Gln Val Ile Phe Ile Thr
            100                 105                 110

Ile Asp Pro Lys Asn Asp Thr Val Glu Lys Leu Lys Glu Phe His Glu
        115                 120                 125

His Phe Asp Ser Arg Ile Gln Met Leu Thr Gly Asn Thr Glu Asp Ile
    130                 135                 140

Asn Gln Ile Ile Lys Asn Tyr Lys Ile Tyr Val Gly Gln Ala Asp Lys
145                 150                 155                     160

Asp His Gln Ile Asn His Ser Ala Ile Met Tyr Leu Ile Asp Lys Lys
                165                 170                 175

Gly Ser Tyr Leu Ser His Phe Ile Pro Asp Leu Lys Ser Gln Glu Asn
            180                 185                 190

Gln Val Asp Lys Leu Leu Ser Leu Val Lys Gln Tyr Leu
        195                 200                 205


<210> 24
<211> 205
<212> PRT
<213> Ehrlichia chaffeensis

<400> 24
Met Lys Val Ile Lys Phe Ile Leu Asn Ile Cys Leu Leu Phe Ala Ala
 1               5                  10                  15

Ile Phe Leu Gly Tyr Ser Tyr Val Thr Lys Gln Gly Ile Phe Gln Val
            20                  25                  30

Arg Asp His Asn Thr Pro Asn Thr Asn Ile Ser Asn Lys Ala Ser Ile
        35                  40                  45

Thr Thr Ser Phe Ser Leu Val Asn Gln Asp Gly Asn Thr Val Asn Ser
    50                  55                  60
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Gln Asp Phe Leu Gly Lys Tyr Met Leu Val Leu Phe Gly Phe Ser Ser
65                  70                  75                  80

Cys Lys Ser Ile Cys Pro Ala Glu Leu Gly Ile Ala Ser Glu Val Leu
                85                  90                  95

Ser Gln Leu Gly Asn Asp Thr Asp Lys Leu Gln Val Ile Phe Ile Thr
            100                 105                 110

Ile Asp Pro Thr Asn Asp Thr Val Gln Lys Leu Lys Thr Phe His Glu
        115                 120                 125

His Phe Asp Pro Arg Ile Gln Met Leu Thr Gly Ser Ala Glu Asp Ile
    130                 135                 140

Glu Lys Ile Ile Lys Asn Tyr Lys Ile Tyr Val Gly Gln Ala Asp Lys
145                 150                 155                 160

Asp Asn Gln Ile Asp His Ser Ala Ile Met Tyr Ile Ile Asp Lys Lys
                165                 170                 175

Gly Glu Tyr Ile Ser His Phe Ser Pro Asp Leu Lys Ser Thr Glu Asn
            180                 185                 190

Gln Val Asp Lys Leu Leu Ser Ile Ile Lys Gln Tyr Leu
        195                 200                 205


<210> 25
<211> 618
<212> DNA
<213> Cowdria ruminantium

<220>
<221> CDS
<222> (1)..(615)

<400> 25
atg aag gct atc aag ttt ata ctt aat cta tgt tta cta ttt gca gca      48
Met Lys Ala Ile Lys Phe Ile Leu Asn Leu Cys Leu Leu Phe Ala Ala
  1               5                  10                  15

att ttt ttg gga tat tct tac ata aca aaa caa ggt ata ttc caa cca      96
Ile Phe Leu Gly Tyr Ser Tyr Ile Thr Lys Gln Gly Ile Phe Gln Pro
            20                  25                  30

aaa tta cac gac tct cct gat gtt aat ata tcg aac aaa gcg gat ata     144
Lys Leu His Asp Ser Pro Asp Val Asn Ile Ser Asn Lys Ala Asp Ile
        35                  40                  45

aat act agc ttt agc tta att aat cag gat ggt att acg ata tct agt     192
Asn Thr Ser Phe Ser Leu Ile Asn Gln Asp Gly Ile Thr Ile Ser Ser
    50                  55                  60

aaa gac ttc ctt gga aaa cat atg tta gtc ctt ttt ggg ttt tct tct     240
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Lys Asp Phe Leu Gly Lys His Met Leu Val Leu Phe Gly Phe Ser Ser
65 70 75 80

tgt aaa act att tgc ccc atg gaa cta ggg tta gca tcc aca att cta 288
Cys Lys Thr Ile Cys Pro Met Glu Leu Gly Leu Ala Ser Thr Ile Leu
85 90 95

gat caa ctt ggc aac gaa tct gac aag tta caa gta gtc ttt ata act 336
Asp Gln Leu Gly Asn Glu Ser Asp Lys Leu Gln Val Val Phe Ile Thr
100 105 110

att gat cca aca aaa gat act gta gaa aca cta aaa gag ttt cac aaa 384
Ile Asp Pro Thr Lys Asp Thr Val Glu Thr Leu Lys Glu Phe His Lys
115 120 125

aat ttt gac tca cgg att caa atg tta aca gga aac att gaa gct att 432
Asn Phe Asp Ser Arg Ile Gln Met Leu Thr Gly Asn Ile Glu Ala Ile
130 135 140

aat caa ata gta caa ggg tac aaa gta tat gta ggt cag cca gac aat 480
Asn Gln Ile Val Gln Gly Tyr Lys Val Tyr Val Gly Gln Pro Asp Asn
145 150 155 160

gat aac caa att aac cat tct gga ata atg tat att gta gac aag aaa 528
Asp Asn Gln Ile Asn His Ser Gly Ile Met Tyr Ile Val Asp Lys Lys
165 170 175

gga gaa tat tta aca cat ttt gta cca gat tta aag tca aaa gag cct 576
Gly Glu Tyr Leu Thr His Phe Val Pro Asp Leu Lys Ser Lys Glu Pro
180 185 190

caa gtg gat aaa tta ctt tct tta att aag cag tat ctt taa 618
Gln Val Asp Lys Leu Leu Ser Leu Ile Lys Gln Tyr Leu
195 200 205

<210> 26
<211> 205
<212> PRT
<213> Cowdria ruminantium

<400> 26
Met Lys Ala Ile Lys Phe Ile Leu Asn Leu Cys Leu Leu Phe Ala Ala
1 5 10 15

Ile Phe Leu Gly Tyr Ser Tyr Ile Thr Lys Gln Gly Ile Phe Gln Pro
20 25 30

Lys Leu His Asp Ser Pro Asp Val Asn Ile Ser Asn Lys Ala Asp Ile
35 40 45

Asn Thr Ser Phe Ser Leu Ile Asn Gln Asp Gly Ile Thr Ile Ser Ser
50 55 60

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Lys Asp Phe Leu Gly Lys His Met Leu Val Leu Phe Gly Phe Ser Ser
65                  70                  75                  80

Cys Lys Thr Ile Cys Pro Met Glu Leu Gly Leu Ala Ser Thr Ile Leu
                85                  90                  95

Asp Gln Leu Gly Asn Glu Ser Asp Lys Leu Gln Val Val Phe Ile Thr
            100                 105                 110

Ile Asp Pro Thr Lys Asp Thr Val Glu Thr Leu Lys Glu Phe His Lys
        115                 120                 125

Asn Phe Asp Ser Arg Ile Gln Met Leu Thr Gly Asn Ile Glu Ala Ile
    130                 135                 140

Asn Gln Ile Val Gln Gly Tyr Lys Val Tyr Val Gly Gln Pro Asp Asn
145                 150                 155                 160

Asp Asn Gln Ile Asn His Ser Gly Ile Met Tyr Ile Val Asp Lys Lys
                165                 170                 175

Gly Glu Tyr Leu Thr His Phe Val Pro Asp Leu Lys Ser Lys Glu Pro
            180                 185                 190

Gln Val Asp Lys Leu Leu Ser Leu Ile Lys Gln Tyr Leu
        195                 200                 205


<210> 27
<211> 981
<212> DNA
<213> Cowdria ruminantium

<220>
<221> CDS
<222> (1)..(978)

<400> 27
atg aag aaa ata ttg gtt acg ttt tta gtt gtt gtt aat gtg ttt tgt      48
Met Lys Lys Ile Leu Val Thr Phe Leu Val Val Val Asn Val Phe Cys
  1               5                  10                  15

aat gct gcc att gct tca act gac tca tca gaa gat aaa cag tat att      96
Asn Ala Ala Ile Ala Ser Thr Asp Ser Ser Glu Asp Lys Gln Tyr Ile
             20                  25                  30

tta att ggt act ggt tct atg act gga gta tat tat cct ata gga ggt     144
Leu Ile Gly Thr Gly Ser Met Thr Gly Val Tyr Tyr Pro Ile Gly Gly
         35                  40                  45

agc ata tgt agg ttt att gca tct gat tat ggt aat gat aat aac agc     192
Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser
     50                  55                  60
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ata gtt tgt tct ata tct tct aca act ggt agc gta tat aat ctt aat 240
Ile Val Cys Ser Ile Ser Ser Thr Thr Gly Ser Val Tyr Asn Leu Asn
65 70 75 80

tct atg cgt tat gca aat atg gat ata ggt att att caa tct gat tta 288
Ser Met Arg Tyr Ala Asn Met Asp Ile Gly Ile Ile Gln Ser Asp Leu
85 90 95

gag tac tat gca tat aat ggt att ggt tta tat gaa aaa atg cca gca 336
Glu Tyr Tyr Ala Tyr Asn Gly Ile Gly Leu Tyr Glu Lys Met Pro Ala
100 105 110

atg agg cat cta aga ata tta tct tca tta cat aaa gaa tat ctt aca 384
Met Arg His Leu Arg Ile Leu Ser Ser Leu His Lys Glu Tyr Leu Thr
115 120 125

att gtt gtt agg gcg aat tct aat ata tca gtt att gat gat ata aaa 432
Ile Val Val Arg Ala Asn Ser Asn Ile Ser Val Ile Asp Asp Ile Lys
130 135 140

ggc aaa aga gtt aat att ggt agt cct ggt act ggt gta aga ata gca 480
Gly Lys Arg Val Asn Ile Gly Ser Pro Gly Thr Gly Val Arg Ile Ala
145 150 155 160

atg tta aaa ttg tta aat gaa aaa gga tgg gga aga aaa gat ttt gct 528
Met Leu Lys Leu Leu Asn Glu Lys Gly Trp Gly Arg Lys Asp Phe Ala
165 170 175

gtt atg gca gaa tta aaa tca tca gag caa gct caa gca tta tgt gat 576
Val Met Ala Glu Leu Lys Ser Ser Glu Gln Ala Gln Ala Leu Cys Asp
180 185 190

aat aaa att gat gtg atg gta gat gtt gtt gga cat cct aat gct gca 624
Asn Lys Ile Asp Val Met Val Asp Val Val Gly His Pro Asn Ala Ala
195 200 205

att caa gaa gca gca gca act tgt gat ata aaa ttt att tct tta gat 672
Ile Gln Glu Ala Ala Ala Thr Cys Asp Ile Lys Phe Ile Ser Leu Asp
210 215 220

gat gat ctc ata gat aaa tta cat act aag tat ccc tat tat aaa agg 720
Asp Asp Leu Ile Asp Lys Leu His Thr Lys Tyr Pro Tyr Tyr Lys Arg
225 230 235 240

gat att att agt ggt gcg tta tac agt aac tta cct gat ata caa act 768
Asp Ile Ile Ser Gly Ala Leu Tyr Ser Asn Leu Pro Asp Ile Gln Thr
245 250 255

gtt tca gta aaa gct tct tta ata aca act act gaa tta agc aat gag 816
Val Ser Val Lys Ala Ser Leu Ile Thr Thr Thr Glu Leu Ser Asn Glu
260 265 270

ttg gcc tat aaa gtt gtt aaa tct ttg gtt agc cat tta cat gaa cta 864
Leu Ala Tyr Lys Val Val Lys Ser Leu Val Ser His Leu His Glu Leu
275 280 285

cat gga att act gga gct ctt aga aat ctt act gta aaa gac atg gta 912
His Gly Ile Thr Gly Ala Leu Arg Asn Leu Thr Val Lys Asp Met Val
290 295 300

cag tca gat att aca cct tta cat gac ggt gca aaa cgt tat tat aag 960
Gln Ser Asp Ile Thr Pro Leu His Asp Gly Ala Lys Arg Tyr Tyr Lys
305 310 315 320

gaa att gga gtt ata aaa taa 981
Glu Ile Gly Val Ile Lys
325

<210> 28
<211> 326
<212> PRT
<213> Cowdria ruminantium

<400> 28
Met Lys Lys Ile Leu Val Thr Phe Leu Val Val Val Asn Val Phe Cys
1 5 10 15

Asn Ala Ala Ile Ala Ser Thr Asp Ser Ser Glu Asp Lys Gln Tyr Ile
20 25 30

Leu Ile Gly Thr Gly Ser Met Thr Gly Val Tyr Tyr Pro Ile Gly Gly
35 40 45

Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser
50 55 60

Ile Val Cys Ser Ile Ser Ser Thr Thr Gly Ser Val Tyr Asn Leu Asn
65 70 75 80

Ser Met Arg Tyr Ala Asn Met Asp Ile Gly Ile Ile Gln Ser Asp Leu
85 90 95

Glu Tyr Tyr Ala Tyr Asn Gly Ile Gly Leu Tyr Glu Lys Met Pro Ala
100 105 110

Met Arg His Leu Arg Ile Leu Ser Ser Leu His Lys Glu Tyr Leu Thr
115 120 125

Ile Val Val Arg Ala Asn Ser Asn Ile Ser Val Ile Asp Asp Ile Lys
130 135 140

Gly Lys Arg Val Asn Ile Gly Ser Pro Gly Thr Gly Val Arg Ile Ala
145 150 155 160

Met Leu Lys Leu Leu Asn Glu Lys Gly Trp Gly Arg Lys Asp Phe Ala
165 170 175

Val Met Ala Glu Leu Lys Ser Ser Glu Gln Ala Gln Ala Leu Cys Asp
180 185 190

Asn Lys Ile Asp Val Met Val Asp Val Val Gly His Pro Asn Ala Ala
195 200 205

Ile Gln Glu Ala Ala Ala Thr Cys Asp Ile Lys Phe Ile Ser Leu Asp
210 215 220

Asp Asp Leu Ile Asp Lys Leu His Thr Lys Tyr Pro Tyr Tyr Lys Arg
225 230 235 240

Asp Ile Ile Ser Gly Ala Leu Tyr Ser Asn Leu Pro Asp Ile Gln Thr
245 250 255

Val Ser Val Lys Ala Ser Leu Ile Thr Thr Thr Glu Leu Ser Asn Glu
260 265 270

Leu Ala Tyr Lys Val Val Lys Ser Leu Val Ser His Leu His Glu Leu
275 280 285

His Gly Ile Thr Gly Ala Leu Arg Asn Leu Thr Val Lys Asp Met Val
290 295 300

Gln Ser Asp Ile Thr Pro Leu His Asp Gly Ala Lys Arg Tyr Tyr Lys
305 310 315 320

Glu Ile Gly Val Ile Lys
325

<210> 29
<211> 519
<212> DNA
<213> Cowdria ruminantium

<220>
<221> CDS
<222> (1)..(516)

<400> 29
atg aat ata ttc aat tat atg cag ata atg cct aat ata agt gtt gat 48
Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp
1 5 10 15

gca ttt gtt gca cct act gct gta att ata ggt gat gtt tgt gta aat 96
Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn
20 25 30

gac aag tgt agc att tgg tat aac tca gta tta cgt gga gat gta ggc 144
Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly
35 40 45

caa att gtt att ggt gta ggt act aat att caa gat ggg aca ata ata 192
Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile
50 55 60

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cat gtt gat agg aaa tat ggt aat acg aat att ggc aaa aag gtt act     240
His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr
 65                 70                  75                  80

att ggg cat ggg tgt ata tta cat gct tgt gag ata caa gat tat gtg     288
Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val
                85                  90                  95

ctt gtt gga atg gga tct att att atg gat aac gtt gtg gtt gaa aag     336
Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys
            100                 105                 110

aat gca atg gtg gct gct gga tca tta gtg gta aga ggt aaa gtt gtg     384
Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val
        115                 120                 125

aaa act ggt gaa tta tgg gct ggt agg cct gca caa ttt tta aga atg     432
Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met
    130                 135                 140

ttg tct agt gat gaa att aaa gag ata agt aaa tct gct gat aac tat     480
Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr
145                 150                 155                 160

ata gag ctt gcc agt gat tac ata act ggt aag ttg taa                 519
Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu
                165                 170
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<210> 30
<211> 172
<212> PRT
<213> Cowdria ruminantium

<400> 30

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Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp
  1               5                  10                  15

Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn
             20                  25                  30

Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly
         35                  40                  45

Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile
     50                  55                  60

His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr
 65                  70                  75                  80

Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val
                 85                  90                  95

Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys
            100                 105                 110
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Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val
        115                 120                 125

Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met
    130                 135                 140

Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr
145                 150                 155                 160

Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu
                165                 170


<210> 31
<211> 753
<212> DNA
<213> Cowdria ruminantium

<220>
<221> CDS
<222> (1)..(750)

<400> 31
atg atg ata aga atc ttt ctt ttg tta ggc tta gta tta tta gta gca      48
Met Met Ile Arg Ile Phe Leu Leu Leu Gly Leu Val Leu Leu Val Ala
1               5                   10                  15

agt ttt cca cta tta aat aac tgg cta tct aat cat tct ggt aag tct      96
Ser Phe Pro Leu Leu Asn Asn Trp Leu Ser Asn His Ser Gly Lys Ser
            20                  25                  30

act aca ttg gat aag gat gca gtt ata tct ata gtt gag gaa tat ata     144
Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile
        35                  40                  45

acc aat tat cct cag agg gta ata gat tta ctt act aca ggc caa gca     192
Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala
    50                  55                  60

caa gca gaa aga gca gag ctt act gaa aat att aaa aaa tat aaa tct     240
Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser
65                  70                  75                  80

gag ctt gaa gat att gca tac cca tct gct ggc aat aaa gac agt aaa     288
Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys
                85                  90                  95

att gca ttt att gag ttc ttc gat tac tct tgt ggt tat tgt aaa atg     336
Ile Ala Phe Ile Glu Phe Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met
            100                 105                 110

atg ttt gaa gat atc aaa caa att ata aaa gat ggt aag gta cgt gtt     384
Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val
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att ttt aga gat ttt cca ata ctt ggg gaa tcg tcg tta aag gct gtt     432
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aaa gca gca ttg gct gta cat ctt atc aat cca agt aaa tac ttg gac     480
Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp
145                 150                 155                 160

ttc tat tat gca gca tta aat cat aaa cag cca ttt aat gat gaa tct     528
Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser
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ata ctt aat ata gtt aaa tca ctt gaa att tca gaa gag gaa ttt aaa     576
Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Glu Phe Lys
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gat tct tta tct aaa aat tct agt act att gat aag atg ata gag tcc     624
Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser
        195                 200                 205

act aga aat ctg gct gag aag tta aat atc aga ggt act cct gct ctt     672
Thr Arg Asn Leu Ala Glu Lys Leu Asn Ile Arg Gly Thr Pro Ala Leu
    210                 215                 220

ata ata ggt gat gca ttc att ggg gga gct gca gat tta tca act tta     720
Ile Ile Gly Asp Ala Phe Ile Gly Gly Ala Ala Asp Leu Ser Thr Leu
225                 230                 235                 240

aga agt aaa ata gta gaa cag cag gaa caa taa                         753
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Ser Phe Pro Leu Leu Asn Asn Trp Leu Ser Asn His Ser Gly Lys Ser
             20                  25                  30

Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile
         35                  40                  45

Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala
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Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser
 65                  70                  75                  80
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Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys
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Ile Ala Phe Ile Glu Phe Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met
100 105 110

Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val
115 120 125

Ile Phe Arg Asp Phe Pro Ile Leu Gly Glu Ser Ser Leu Lys Ala Val
130 135 140

Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp
145 150 155 160

Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser
165 170 175

Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Glu Phe Lys
180 185 190

Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser
195 200 205

Thr Arg Asn Leu Ala Glu Lys Leu Asn Ile Arg Gly Thr Pro Ala Leu
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1 5 10 15

gca gga gca ata tct att ggg ata ata gca ttt aac aaa tta cca tat 96
Ala Gly Ala Ile Ser Ile Gly Ile Ile Ala Phe Asn Lys Leu Pro Tyr
20 25 30

aaa aat acc ttg cgt aat tgt tat aca gtt aaa gca ttt ttc tca aat 144
Lys Asn Thr Leu Arg Asn Cys Tyr Thr Val Lys Ala Phe Phe Ser Asn
35 40 45

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gta gat ggg ttg gac ata gga gat gaa gta aca ata tca gga gta aaa    192
Val Asp Gly Leu Asp Ile Gly Asp Glu Val Thr Ile Ser Gly Val Lys
     50                  55                  60

ata ggt aca gta act tca ata tca ttg aat gaa agc tat act cct ata    240
Ile Gly Thr Val Thr Ser Ile Ser Leu Asn Glu Ser Tyr Thr Pro Ile
 65                  70                  75                  80

gta aca atg tgc ata cag aaa aat atc tta cta cct tca gat agt tca    288
Val Thr Met Cys Ile Gln Lys Asn Ile Leu Leu Pro Ser Asp Ser Ser
                 85                  90                  95

gca tct ata tta aac agc aat atg tta gga aaa aag cac att gat atc    336
Ala Ser Ile Leu Asn Ser Asn Met Leu Gly Lys Lys His Ile Asp Ile
            100                 105                 110

gaa ctt gga tca gat caa gaa gtc atc gta agt gaa ggt tta ata gaa    384
Glu Leu Gly Ser Asp Gln Glu Val Ile Val Ser Glu Gly Leu Ile Glu
        115                 120                 125

cat aca cat tca gat tta agt ttc aat gca att att gct aaa ata ata    432
His Thr His Ser Asp Leu Ser Phe Asn Ala Ile Ile Ala Lys Ile Ile
    130                 135                 140

gat tca ctt att aag tag                                            450
Asp Ser Leu Ile Lys
145
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<210> 34
<211> 149
<212> PRT
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  1               5                  10                  15

Ala Gly Ala Ile Ser Ile Gly Ile Ile Ala Phe Asn Lys Leu Pro Tyr
             20                  25                  30

Lys Asn Thr Leu Arg Asn Cys Tyr Thr Val Lys Ala Phe Phe Ser Asn
         35                  40                  45

Val Asp Gly Leu Asp Ile Gly Asp Glu Val Thr Ile Ser Gly Val Lys
     50                  55                  60

Ile Gly Thr Val Thr Ser Ile Ser Leu Asn Glu Ser Tyr Thr Pro Ile
 65                  70                  75                  80

Val Thr Met Cys Ile Gln Lys Asn Ile Leu Leu Pro Ser Asp Ser Ser
                 85                  90                  95

Ala Ser Ile Leu Asn Ser Asn Met Leu Gly Lys Lys His Ile Asp Ile
            100                 105                 110
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Glu Leu Gly Ser Asp Gln Glu Val Ile Val Ser Glu Gly Leu Ile Glu
        115                 120                 125

His Thr His Ser Asp Leu Ser Phe Asn Ala Ile Ile Ala Lys Ile Ile
    130                 135                 140

Asp Ser Leu Ile Lys
145
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INTERNATIONAL SEARCH REPORT

Intern al Application No
PCT/US 00/10886

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/31 C07K14/29 A61K39/02 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 16554 A (UNIV FLORIDA) 23 April 1998 (1998-04-23) the whole document ---	1-24
X	BOWIE MICHAEL V ET AL: "Potential value of major antigenic protein 2 for serological diagnosis of heartwater and related Ehrlichial infections." CLINICAL AND DIAGNOSTIC LABORATORY IMMUNOLOGY, vol. 6, no. 2, March 1999 (1999-03), pages 209-215, XP000939015 ISSN: 1071-412X the whole document ---	1-4, 7-13, 21-24

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
5 September 2000	22 12 2000

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	ANDRES S.M.

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 00/10886

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	NYIKA A ET AL.: "A DNA vaccine protects mice against the rickettsial agent Cowdria ruminantium." PARASITE IMMUNOLOGY (OXFORD), vol. 20, no. 3, March 1998 (1998-03), pages 111-119, XP000939081 ISSN: 0141-9838 the whole document ---	1-4, 6-14, 17-19
X	MAHAN S M ET AL: "Molecular cloning of a gene encoding the immunogenic 21 kDa protein of Cowdria ruminantium." MICROBIOLOGY (READING), vol. 140, no. 8, 1994, pages 2135-2142, XP000939016 the whole document -----	1-4, 7-13, 21-24

1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/10886

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

see FURTHER INFORMATION sheet PCT/ISA/210

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-24

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claims 10 to 19 are directed to a method of treatment of the human/animal body, and claim 20 (as far as an in vivo method is concerned) is directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-24

1.1. Claims: 1-2,6-7,10-11,17-19,21-22 (all partially)
A composition comprising a polynucleotide encoding an antigen from Rickettsia spp. and methods for using it in protection of a host against a disease or death, or in diagnostic.

1.2. Claims: 1-4,6-13,17-24 (all partially), and claims 5, 15 (totally)

Compositions comprising SEQ IDs 3,4; 7,14; 8,15; 9,16; 10,17; 11,18 and 22,24 (corresponding to the MAP1, VSA1 to VSA5 and MAP2 antigens from Ehrlichia chaffeensis) and methods for using them in protection of a host against a disease or death, or in diagnostic.

1.3. Claims: 1-4,6-13,17-24 (all partially)
Compositions comprising SEQ IDs 12,19; 13,20 and 21,23 (corresponding to the VSA1, VSA2 and MAP2 antigens from Ehrlichia canis) and methods for using them in protection of a host against a disease or death, or in diagnostic.

1.4. Claims: 1-4,6-13,17-19, 21-24 (all partially) and claim 16 (totally)

A compositions comprising SEQ IDs 4 and 5 (corresponding to the MSP-4 antigen from Anaplasma marginale) and methods for using it in protection of a host against a disease or death, or in diagnostic.

1.5. Claims: 1-4,6-13,17-19, 21-24 (all partially) and claim 14 (totally)

Compositions comprising SEQ IDs 1,2 and 25,26 (corresponding to the antigens MAP1 and MAP2 from Cowdria ruminantium) and methods for using them in protection of a host against a disease or death, or in diagnostic.

2. Claims: 1-4,6-13,17-19,21-24 (all partially)

A composition comprising SEQ IDs 27 and 28 (corresponding to the 1hworf3 antigen from Cowdria ruminantium) and methods

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

for using it in protection of a host against a disease or death, or in diagnostic.

3. Claims: 1-4,6-13,17-19,21-24 (all partially)

A composition comprising SEQ IDs 29 and 30 (corresponding to the 4hworf1 antigen from Cowdria ruminantium) and methods for using it in protection of a host against a disease or death, or in diagnostic.

4. Claims: 1-4,6-13,17-19,21-24 (all partially)

A composition comprising SEQ IDs 31 and 32 (corresponding to the 18hworf1 antigen from Cowdria ruminantium) and methods for using it in protection of a host against a disease or death, or in diagnostic.

5. Claims: 1-4,6-13,17-19,21-24 (all partially)

A composition comprising SEQ IDs 33 and 34 (corresponding to the 3gdorf3 antigen from Cowdria ruminantium) and methods for using it in protection of a host against a disease or death, or in diagnostic.

Please note that all inventions mentioned under item 1, although not necessarily linked by a common inventive concept, could be searched without effort justifying an additional fee.

INTERNATIONAL SEARCH REPORT

ormation on patent family members

Interr ial Application No
PCT/US 00/10886

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9816554 A	23-04-1998	US 6025338 A	15-02-2000
		AU 4913097 A	11-05-1998
		ZA 9709320 A	16-03-1999